

TABLE 1
Document Number 1650775

GLGC Comparison ID	Nucleotide Sequence ID	GenBank AccID	Pathways	Known Gene Name	Unigene Cluster Title
19 N		1729 NM_017258		B-cell translocation gene 1, anti-proliferative	B-cell translocation gene 1, anti-proliferative
20 L,N		1729 NM_017258		B-cell translocation gene 1, anti-proliferative	B-cell translocation gene 1, anti-proliferative
43 E,P	1688 NM_022287	Glycosaminoglycan degradation	HMMalpha-L-iduronidase	Rattus norvegicus sulfate anion transporter (sak-1) mRNA, complete cds	
55 O	1535 NM_012511	Oxidative phosphorylation	ATPase, Cu++ transporting, beta polypeptide (same as Wilson disease)	ATPase, Cu++ transporting, beta polypeptide (same as Wilson disease)	
64 H	1620 NM_016991		Adrenergic, alpha 1B, receptor	Adrenergic, alpha 1B, receptor	
72 F	1420 M57263		Hsp PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE K	Rat protein-glutamine gamma-glutamyltransferase mRNA, complete cds	
90 E	1454 U20796			Rattus norvegicus nuclear receptor Rev-ErbA-beta mRNA, partial cds	
134 A	1346 D87839	Alanine and aspartate metabolism, Butanoate metabolism, Glutamate metabolism, Propanoate metabolism, beta-Alanine metabolism	Hs-4-aminobutyrate aminotransferase	Rattus norvegicus mRNA for beta-alanine oxoglutarate aminotransferase, complete cds	
135 A	1346 D87839	Alanine and aspartate metabolism, Butanoate metabolism, Glutamate metabolism, Propanoate metabolism, beta-Alanine metabolism	Hs-4-aminobutyrate aminotransferase	Rattus norvegicus mRNA for beta-alanine oxoglutarate aminotransferase, complete cds	

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GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	
154 P_Q	1712 NM_022849		cpr-ductin		Rattus norvegicus ebnerin mRNA, complete cds	
155 P	1712 NM_022849		cpr-ductin		Rattus norvegicus ebnerin mRNA, complete cds	
164 H	538 AI010480		Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, Pyruvate metabolism	Malate dehydrogenase 2, NAD (mitochondrial)	Rat mRNA for mitochondrial malate dehydrogenase (EC 1.1.1.37)	
228 D	1452 U20194				Rattus norvegicus complement C8 beta (C8b) mRNA, partial cds	
291 O	1538 NM_012522		Glycine, serine and threonine metabolism, Methionine metabolism, Selenocompound metabolism	Cystathione beta synthase	Cystathione beta synthase	
330 R	1251 AI235460				Rattus norvegicus synapse-associated protein 102 mRNA, complete cds	
347 J	1443 U01914				Rattus norvegicus AKAP56 mRNA, partial cds	
351 A	1720 NM_024127			HHs growth arrest and DNA-damage-inducible, alpha	Rattus norvegicus GADD45 mRNA, complete cds	
352 A_J	1720 NM_024127			HHs growth arrest and DNA-damage-inducible, alpha	Rattus norvegicus GADD45 mRNA, complete cds	
353 A,B,C,J	1720 NM_024127			HHs growth arrest and DNA-damage-inducible, alpha	Rattus norvegicus GADD45 mRNA, complete cds	
354 A,J,Q	1720 NM_024127			HHs growth arrest and DNA-damage-inducible, alpha	Rattus norvegicus GADD45 mRNA, complete cds	

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GLGC Companion ID	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title	
355 N		1600 NM_013086		CAMP responsive element modulator;transcriptional repressor	CAMP responsive element modulator	
356 N		1658 NM_017334		CREM	CAMP responsive element modulator	
360 R		1728 NM_012894		CAMP responsive element modulator	RNA editing deaminase of glutamate receptors	
372 F.M		1482 U94708		RNA editing deaminase of glutamate receptors	Rattus norvegicus prostaglandin E receptor EP2 subtype mRNA, complete cds	
373 P		1578 NM_012833		Canalicular multispecific organic anion transporter	Canalicular multispecific organic anion transporter	
384 O		1457 U25137			Rattus norvegicus alternatively spliced signal transducer and regulator of transcription 5a2 (STA5a2) mRNA, partial cds	
396 M		1464 U49694		Hsp:CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE	Rattus norvegicus brain cytosolic acyl coenzyme A thioester hydrolase mRNA, complete cds	
397 S		1614 NM_013214		acyl-CoA hydrolase	Rattus norvegicus brain cytosolic acyl coenzyme A thioester hydrolase mRNA, complete cds,acyl-CoA hydrolase	
402 N		1734 NM_022403	Tryptophan metabolism	HH:tryptophan 2,3-dioxygenase	Rat tryptophan-2,3-dioxygenase mRNA, complete cds	
466 L		1517 X81395		Hsp:LIVER CARBOXYL ESTERASE 3 PRECURSOR	R.norvegicus mRNA for pl 5.5 esterase (ES-3)	

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
475 F			1224 AI233828		Cytochrome P450, subfamily I (aromatic compound-inducible), member A1 (C6, form c)	ESTs, Moderately similar to LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR [M.musculus]
488 F		1350 E00717		Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily I (aromatic compound-inducible), member A1 (C6, form c)	Cytochrome P450, subfamily I (aromatic compound-inducible), member A1 (C6, form c)
489 F			1540 NM_012540	Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily I (aromatic compound-inducible), member A1 (C6, form c)	Cytochrome P450, subfamily I (aromatic compound-inducible), member A1 (C6, form c)
494 G			1561 NM_012880		Superoxide dimutase 3	Superoxide dimutase 3
498 C			402 AA956278			ESTs
556 A,E			1575 NM_012803		Protein C	Protein C
563 M			1536 NM_012516		Complement component 4 binding protein, alpha	Complement component 4 binding protein, alpha
573 A			1169 AI232087		R.nonvegicus mRNA for (S)-2-hydroxy acid oxidase	R.nonvegicus mRNA for (S)-2-hydroxy acid oxidase, Rattus nonvegicus clone BB.1.4, unknown Glu+Pro dipeptide repeat protein mRNA, complete cds, calpastatin heavy chain
						ESTs
574 H,I			1682 NM_019905			
633 A,G			1146 AI231127		Hsp60/GLUTATHIONE S-TRANSFERASE YC-1	Rat liver glutathione S-transferase Yc subunit mRNA, complete cds
634 P			1381 K01932	Glutathione metabolism		Rat liver glutathione S-transferase Yc subunit mRNA, complete cds
635 P			1515 X78848			
650 J			1607 NM_013134	Sterol biosynthesis	A reductase	3-hydroxy-3-methylglutaryl-Coenzyme A reductase

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GLGC ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number
651 J		1607 NM_013134	Sterol biosynthesis	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	1650773
671 B		1445 U04808			Rattus norvegicus Sprague-Dawley putative G-protein coupled receptor (GCR) mRNA, complete cds	
672 O		1492 X13722			Rat mRNA for LDL-receptor	
682 P		1627 NM_017051			Superoxide dimutase 2, mitochondrial	
699 M,P		1465 U55765			Rattus norvegicus RASP1 mRNA, complete cds	
729 O		1429 M85762			Rattus norvegicus GABA transporter GAT-2 mRNA, complete cds	
761 A		41 AA817685			Rattus norvegicus mRNA for cytochrome b5	
794 A,D,E,G		1472 J88168	Tryptophan metabolism	I(Hs-)kynureninase (L-kynurenone hydrolase)	Rattus norvegicus L-kynurenone hydrolase mRNA, complete cds	
809 J		1451 U17035			Rattus norvegicus interferon inducible protein 10 (IP-10) mRNA, complete cds	
811 A		1342 D63704	Pantothenate and CoA biosynthesis, Pyrimidine metabolism,beta-Alanine metabolism	I(Hs-)dihydropyrimidinase	Rat mRNA for dihydropyrimidinase, complete cds	
812 A		1342 D63704	Pantothenate and CoA biosynthesis,Pyrimidine metabolism,beta-Alanine metabolism	I(Hs-)dihydropyrimidinase	EST, Highly similar to DPYS_RAT DIHYDROPYRIMIDINASE [R,norvegicus], Rat mRNA for dihydropyrimidinase, complete cds	

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GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
820 E	238 AA692395		Fructose and mannose metabolism, Glycolysis/Gluconeogenesis, Pentose phosphate cycle	Aldolase B, fructose-biphosphate	Rattus norvegicus laminin-5-alpha 3 chain mRNA, complete cds
825 A	381 AA946108				Rattus norvegicus fatty acid amide hydrolase mRNA, complete cds
851 A	1721 NM_024132		fatty acid amide hydrolase		Rattus norvegicus INS-1 winged helix mRNA, complete cds
906 K	1480 U83112			BcI2-associated X protein	BcI2-associated X protein
912 A	1467 U59194			Tumor-associated glycoprotein pE4	Tumor-associated glycoprotein pE4
923 A,J	1632 NM_017076				Rattus norvegicus mRNA for PS-PLA ₁ , complete cds
945 P	1349 D88666				Rattus norvegicus PSD-95/SAP90-associated protein 2 mRNA, complete cds
955 M	1471 U67138			Lectin, galactose binding, soluble 9 (Galactin-9)	Lectin, galactose binding, soluble 9 (Galactin-9)
958 I,Q	1591 NM_012977			Glutathione S-transferase 1 (liver)	Glutathione S-transferase 1 (liver)
961 A	1573 NM_012796		Glutathione metabolism	Cytochrome P450 (cholesterol hydroxylase 7 alpha)	Cytochrome P450 (cholesterol hydroxylase 7 alpha)
1007 A	1589 NM_012942		Bile acid biosynthesis	Transporter 1, ABC (ATP binding cassette)	R.norvegicus mtp1 mRNA
1037 I	1500 X57523			Cytochrome P450, subfamily 1F, polypeptide 1	Cytochrome P450, subfamily 1F, polypeptide 1
1099 A	1678 NM_019303				Rattus norvegicus neuron-specific enolase (NSE) mRNA, complete cds
1114 N	586 AJ029917				

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GLDC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
1126 A,I		1143 AI231007			Rattus norvegicus cca1 mRNA, complete cds	
1141 E,Q		1505 X59601			Rat mRNA for plectin	
1169 E,H		1008 Al177161			Rattus norvegicus NF-E2-related factor 2 mRNA, complete cds	
1173 A		1661 NM_019184	Cytochrome P450, subfamily 1C (mephenytoin 4-hydroxylase)	Cytochrome P450, subfamily 1C (mephenytoin 4-hydroxylase)	Cytochrome P450, subfamily 1C (mephenytoin 4-hydroxylase)	
1174 N		1661 NM_019184	Cytochrome P450, subfamily 1C (mephenytoin 4-hydroxylase)	Cytochrome P450, subfamily 1C (mephenytoin 4-hydroxylase)	Cytochrome P450, subfamily 1C (mephenytoin 4-hydroxylase)	
1175 A,E,M		1661 NM_019184	Cytochrome P450, subfamily 1C (mephenytoin 4-hydroxylase)	Cytochrome P450, subfamily 1C (mephenytoin 4-hydroxylase)	Cytochrome P450, subfamily 1C (mephenytoin 4-hydroxylase)	
1183 J		485 AF013144		Hsp:DUAL SPECIFICITY PROTEIN PHOSPHATASE 5	Rattus norvegicus MAP-kinase phosphatase (cpq21) mRNA, complete cds	
1221 B,F,Q		1326 D11445			Rattus norvegicus mRNA for gro, complete cds	
1223 E		1423 M75281			Rat crystallin S (CrysS) gene, complete cds	
1246 A		1569 NM_012770	Purine metabolism	Guanylate cyclase, soluble, beta 2 (GTP pyrophosphate - lyase)	Guanylate cyclase, soluble, beta 2 (GTP pyrophosphate - lyase)	
1258 I		1611 NM_013185		Hemopoietic cell tyrosine kinase	Hemopoietic cell tyrosine kinase	
1271 Q		1384 L07073			Rat clathrin-associated adaptor protein homolog (p47A) mRNA, complete cds	
1279 F		1477 UT5916			Rattus norvegicus zonula occludens 2 protein (ZO-2) mRNA, partial cds	
1306 J		1636 NM_017127	Glycerolipid metabolism	choline kinase	choline kinase	
1394 G		1461 U37099		choline kinase	Rattus norvegicus GTP-binding protein (rab 3C) mRNA, complete cds	

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GLGC Comparison ID	Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
1399	C,D,G	1623	NM_017006	Glutathione metabolism, Riboflavin metabolism, Pentose phosphate cycle	Glucose-6-phosphate dehydrogenase	Glucose-6-phosphate dehydrogenase
1409	A	560	AJ012802	Pyruvate metabolism	HHs:hydroxacyl glutathione hydrolase	Rattus norvegicus round spermatid protein RSP29 gene, complete cds
1411	C,D	920	AJ172075			ESTs
1426	Q	1528	Z48225	Histidine metabolism, Phenylalanine metabolism, Tryptophan metabolism, Tyrosine metabolism	Dopa decarboxylase (aromatic L-amino acid decarboxylase) proteasome (prosome, macropain) subunit, alpha type 4 Keratin 8	Rattus norvegicus mRNA for protein synthesis initiation factor elf-2B delta subunit
1430	M	1542	NM_012545		Dopa decarboxylase (aromatic L-amino acid decarboxylase) proteasome (prosome, macropain) subunit, alpha type 4	Dopa decarboxylase (aromatic L-amino acid decarboxylase) proteasome (prosome, macropain)
1447	F	1651	NM_017281		Keratin 8	
1460	C,D	1439	S76054			
1475	J	1386	L16764		Heat shock protein 70-1,S100 calcium binding protein A1	Rattus norvegicus S100A1 gene,Rattus norvegicus heat shock protein 70 (HS70) mRNA, complete cds
1478	A	1566	NM_012744	Alanine and aspartate metabolism,Citrate cycle (TCA cycle),Pyruvate metabolism	Pyruvate carboxylase	Pyruvate carboxylase
1479	A,G,K		1566	Alanine and aspartate metabolism,Citrate cycle (TCA cycle),Pyruvate metabolism	Pyruvate carboxylase	Pyruvate carboxylase
1501	A,C,F,H		690	AJ072634		Rattus norvegicus cytokeratin-18 mRNA, partial cds

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GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
1507 B,Q	1105 NM_0129235			ESTs	organic cationic transporter-like 1
1510 Q	1646 NM_017224			organic cationic transporter-like 1	Tropomyocin 4
1514 B	1559 NM_012678			Tropomyocin 4	Interleukin 18
1520 H	1659 NM_019165			Interleukin 18	Tumor necrosis factor receptor
1521 B,Q	1601 NM_013091			Tumor necrosis factor receptor	Ryudocan/syndecan 2
1529 A,G	1599 NM_013082		Bile acid biosynthesis, Taurine and hypotaurine metabolism	bile acid-Coenzyme A dehydrogenase; amino acid n-acyltransferase	bile acid-Coenzyme A dehydrogenase; amino acid n-acyltransferase
1531 A	1655 NM_017300				Rat kidney Zn-peptidase aminopeptidase N mRNA, complete cds
1538 E	493 AF039890		Leucine arylaminopeptidase 1		Kynureine aminotransferase II
1542 G,H	1643 NM_017193		Kynureine aminotransferase II		Glycine methyltransferase
1551 K	1633 NM_017084		Glycine methyltransferase	Sialophorin (gpl115, leukosianin, CD13)	Sialophorin (gpl115, leukosianin, CD13)
1554 I	625 AI045440		Complement component 4 binding protein, beta	Complement component 4 binding protein, beta	Complement component 4 binding protein, beta
1561 A,M,O	1621 NM_016995			Rattus norvegicus kallistatin mRNA, complete cds	Rattus norvegicus kallistatin mRNA, complete cds
1562 F,G	267 AA893552			Rattus norvegicus Sprague/Dawley PHAS-1 mRNA, complete cds	Rattus norvegicus Sprague/Dawley PHAS-1 mRNA, complete cds
1571 I	1446 U05014			Rattus norvegicus Sprague/Dawley PHAS-1 mRNA, complete cds	Rattus norvegicus Sprague/Dawley PHAS-1 mRNA, complete cds
1572 Q	1046 AI178828			Rat small nuclear ribonucleoparticle-associated protein (snRNP) mRNA, complete cds, clone Sm151	Rat small nuclear ribonucleoparticle-associated protein (snRNP) mRNA, complete cds, clone Sm151
1579 R	1512 X73411				

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GLGC Comparison ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name*	Unigene Cluster ID*
1583 A		1448	U07201	Alanine and aspartate metabolism, Nitrogen metabolism	Asparagine synthetase	Rattus norvegicus GADD153 mRNA, complete cds
1598 C,J		1722	NM_024134		DNA-damage inducible transcript 3	Rattus norvegicus survival motor neuron (smn) mRNA, complete cds
1610 C		1703	NM_022509	Cell surface glycoprotein CD44 (hyaluronate binding protein)	Cell surface glycoprotein CD44 (hyaluronate binding protein)	
1625 I		1588	NM_012924	Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase	
1641 E		1354	E03428	Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase	
1644 G		208	AA891068	Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase	
1653 G		1222	A1233806	Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase	
1661 B,E		1459	U26397	Inositol phosphate metabolism	Rattus norvegicus inositol polyphosphate-4-phosphatase, type I, 107KD	Rattus norvegicus inositol polyphosphate 4-phosphatase mRNA, complete cds
1690 A,E		46	AA817829		ES1's, Highly similar to MEK binding partner 1 [M.musculus]	ES1's, Highly similar to TBB1_RAT
1700 P		1486	X03369		TUBULIN BETA CHAIN [R.norvegicus], Rat mRNA for beta-tubulin T beta15	TUBULIN BETA CHAIN [R.norvegicus], Rat mRNA for beta-tubulin T beta15
1727 C,J		482	AF001417	tubulin, beta 2	Rattus norvegicus zinc finger protein mRNA, complete cds	Rattus norvegicus zinc finger protein mRNA, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
				Bile acid biosynthesis, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Phenylalanine metabolism, Valine, leucine and isoleucine degradation	H3-hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/fatty acyl-Coenzyme A thioesterase (trifunctional protein), beta subunit	Rat mRNA for mitochondrial long-chain 3-ketoacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, complete cds
1728 E,S		1332 D16479	1657 NM_017327		GTP-binding protein	GTP-binding protein
.1749 K		1462 U39208		Prostaglandin and leukotriene metabolism	H3s-cytochrome P450, subfamily IVF, polypeptide 2	Rattus norvegicus cytochrome P450 4F6 (CYP4F6) mRNA, complete cds
1753 A		1586 NM_012918			Calcium channel alpha 1A	Calcium channel alpha 1A
1777 P		1392 L24207			Cytochrome P450, subfamily IIIA, polypeptide 3	Cytochrome P450, subfamily IIIA, polypeptide 3
1795 B,K,Q		1392 L24207			Cytochrome P450, subfamily IIIA, polypeptide 3	Cytochrome P450, subfamily IIIA, polypeptide 3
1796 B,K		1392 L24207			ESFs	ESFs
1802 H		47 AA0117841				Rattus rattus guanine nucleotide-releasing protein (m34) mRNA, complete cds
1805 N		508 AU007824				Rat mRNA for alpha-2u globulin-related protein
1809 F		391 AA946503				Protein-tyrosine phosphatase
1841 C,N		1555 NM_012637				Protein-tyrosine phosphatase
1843 N,Q		1555 NM_012637				Protein-tyrosine phosphatase
1844 A,N		1555 NM_012637				ESTs Protein-tyrosine phosphatase
1854 M		1382 KU02814			K-kininogen, differential splicing leads to HMW KngK-T-kininogen	K-kininogen, differential splicing leads to HMW KngK-T-kininogen

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GLoc ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
1858 S		1524	Y09333	Fructose and mannose metabolism	acyl-CoA thioesterase 1, cytosolic	R.norvegicus mRNA for mitochondrial very-long-chain acyl-CoA thioesterase Rattus norvegicus mRNA for acyl-CoA hydrolase, complete cds
1877 A		1513	X74593	Sorbitol dehydrogenase	Sorbitol dehydrogenase	Rattus norvegicus mRNA for proteasomal ATPase 7 (Tat-binding protein 7), complete cds
1884 L		1340	D50695	Glycerolipid metabolism, Phospholipid degradation, Prostaglandin and leukotriene metabolism	phospholipase A2, group IIA (platelets, synovial fluid)	Rattus norvegicus mRNA for phospholipase A2 precursor, complete cds
1893 P		1495	X51529			ESTs
1900 A,B,L		48	AA817849			ESTs
1901 L		48	AA817849			ESTs
1903 L		1013	A1177377			ESTs
1919 H		815	A137856	P450 (cytochrome) oxidoreductase	P450 (cytochrome) oxidoreductase	Rat NADPH-cytochrome P-450 oxidoreductase mRNA, complete cds
1920 H		1397	M10068	P450 (cytochrome) oxidoreductase	P450 (cytochrome) oxidoreductase	Rat NADPH-cytochrome P-450 oxidoreductase mRNA, complete cds
1921 H		1351	E01524	P450 (cytochrome) oxidoreductase	Hsp[PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOCYPE 2, MITOCHONDRIAL PRECURSOR	Rattus norvegicus pyruvate dehydrogenase kinase 2 subunit (PDK2) mRNA, complete cds
1929 A		1449	U10357			Rattus norvegicus pyruvate dehydrogenase kinase 2 subunit p45 (PDK2) mRNA, complete cds
1930 L		410	AA857202			

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UniGene Cluster Title	Known Gene Name	Pathways	GenBank Accession ID	Nucleotide Sequence ID	Comparison Code	Gl/Go ID
Hras-revertant gene 107	Hras-revertant gene 107	Glycine, serine and threonine metabolism, Methionine metabolism	1628 NM_017060	1957 K		
Rattus norvegicus betaine homocysteine methyltransferase (BHMT) mRNA, complete cds	HMm:betaine-homocysteine methyltransferase		492 AF038870	1995 N		
R.norvegicus mRNA for cytosolic epoxide hydrolase						
Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)	Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)		1716 NM_022936	2006 E		
Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)	Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)		1610 NM_013173	2011 P		
Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)	Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)		1610 NM_013173	2012 P		
Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)	Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)		1610 NM_013173	2013 P		
ESTs			721 AI010921	2042 Q,R		
ESTs			1125 AI230171	2043 E,H		
ESTs			417 AA963369	2049 J		
ESTs			418 AA963372	2051 S		
ESTs			1084 AI227769	2065 I		
ESTs			565 AI013667	2101 R		
ESTs, Weakly similar to AF077030_1 hypothetical 43.2 kDa protein [H.sapiens]			750 AI103560	2111 A		
Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds			423 AA964275	2113 S		
ESTs			1475 U75404	2117 R		
Rattus norvegicus Cdk102 mRNA				2153 E		

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2154 R		1223	AI233818			ESTs	
2164 A		781	AI111413			ESTs	
2190 S		420	AA864004			ESTs	
2196 A		776	AI105243			ESTs	
2216 R		912	AI171745			ESTs	
2264 A		821	AI144714			ESTs	
2280 H		421	AA864139			EST	
2292 E		714	AI101362			ESTs	
2310 M		587	AI028969			ESTs	
2326 L		432	AA864892		ESTs, Highly similar to CA14_MOUSE COLLAGEN ALPHA 1(V) CHAIN PRECURSOR [M.musculus]		
2335 A		424	AA864302		ESTs		
2339 E		1162	AI231798		ESTs		
2342 E		425	AA864236		EST		
2350 D		426	AA864368		ESTs, Highly similar to TGT_HUMAN QUELINE TRNA-RIBOSYLTRANSFERASE [H.sapiens]		
2354 L		454	AA997763		ESTs, Highly similar to hypothetical protein [H.sapiens]		
2359 N		998	AI177029		ESTs, Highly similar to JU0227 protein-tyrosine kinase [M.musculus]		
2368 N		504	AF095741		Rattus norvegicus MG87 mRNA, complete cds		
2372 A_L		1150	AI230373		ESTs		
2373 O		428	AA864455		ESTs		
2383 A_E		429	AA864514		EST		
2457 S		431	AA864752		EST		
2484 A_O		761	AI104675		ESTs		

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2505 A,G		1549 NM_012597		Glycerolipid metabolism	Lipase, hepatic	
2506 E		524 A1009341				ESTs
2532 A		975 A1176590				ESTs
2536 A		978 A1176616				ESTs
2555 B,C,Q		1590 NM_012967		Intercellular adhesion molecule 1	Intercellular adhesion molecule 1	
2569 A,C,F,K,R		435 AA965122				ESTs
2576 A		226 AA691884				ESTs
2587 G		1170 A1232103				ESTs
2594 L		1241 A1234843			Yeast LPG22 protein [C.elegans]	
2615 C,J		1109 A1229318				ESTs
2628 J		1551 NM_012603		Avian myelocytomatisis viral (v-myc) oncogene homolog	Avian myelocytomatisis viral (v-myc) oncogene homolog	
2629 J		1551 NM_012603		Avian myelocytomatisis viral (v-myc) oncogene homolog	Avian myelocytomatisis viral (v-myc) oncogene homolog	
2655 B,N,Q		343 AA943886			Rattus norvegicus protein kinase SnRK (Snk) mRNA, complete cds	
2667 G		1568 NM_012766		Tocopherol transfer protein alpha	Tocopherol transfer protein alpha	ESTs
2691 R		434 AA965075				
2696 A		1737 NM_022515			R.norvegicus (Sprague Dawley) mRNA for ribosomal protein L24	
2727 H		252 AA892918				ESTs
2736 Q		1537 NM_012519		Ca++/calmodulin-dependent protein kinase II, delta subunit	Ca++/calmodulin-dependent protein kinase II, delta subunit	
2744 I		1347 D87991				ESTs, Highly similar to UGTr1
2757 L		456 AA897851				[M.musculus]
2762 A		350 AA944165			ESTs, Highly similar to C10	
						[M.musculus]

TABLE 1

Document Number 1650275					
GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc. ID	Pathways	Known Gene Name	Unigene Cluster Title
2763 E	1173	AI232269			ESTs
2781 I	50	AA817925			ESTs
2788 J	939	AI176513		Rattus norvegicus mRNA for phocine protein	
2799 A	568	AI013778		ESTs	
2801 F	1345	D85435		Rattus norvegicus mRNA for protein kinase C delta-bindig protein, complete cds	
2802 F	1345	D85435		Rattus norvegicus mRNA for protein kinase C delta-bindig protein, complete cds	
2803 L	437	AA996451		ESTs	
			Butanoate metabolism, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation	HMM:3-hydroxy-3-methylglutaryl- Coenzyme A lyase	R.norvegicus mRNA for 3-hydroxy-3- methylglutaryl CoA lyase
2813 S	385	AA945052			ESTs
2818 C,D,F	1056	AI179144			
2838 D	665	AI070511			
2853 I	1579	NM_012838		Cystatin beta	[M.musculus]
2854 I	1579	NM_012838		Cystatin beta	Cystatin beta
2868 E	1171	AI232209			ESTs
2897 C,D	51	AA818039			ESTs
2901 A	603	AI043752			ESTs
2905 A,B	438	AA996727			ESTs
2911 A	567	AI030835			ESTs
2915 R	439	AA996782			ESTs
2932 R	1204	AI233288			ESTs

TABLE 1 Document Number 1650775

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
2933 E		1665	NM_019204		ESTs, Highly similar to beta-site APP cleaving enzyme [R.norvegicus]	
2938 C		440	AA996683		ESTs	
2993 A		971	AI176492		ESTs, Highly similar to AF188297_1 TGF-beta receptor binding protein [M.musculus]	
3023 G		885	AI170795		EST, Weakly similar to CBP_B RAT CARBOXYPEPTIDASE B PRECURSOR [R.norvegicus]	
3062 D		468	AA998857		ESTs	
3073 A,E,O		1213	AI233494		ESTs	
3074 A,E,O		1213	AI233494		ESTs	
3075 A,O		1213	AI233494		ESTs	
3080 H		242	AA992553	HHs signal transducer and activator of transcription 1, p110	RAitis norvegicus signal transducer and activator of transcription 1 (Stat1) mRNA, complete cds	
3091 E		1260	AI236027		ESTs	
3099 S		1113	AI229680	Oxidative phosphorylation, Ubiquinone biosynthesis	HHs:NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase) NDUF53 subunit [H.sapiens]	
3121 A,B,E		510	AI008160		ESTs, Moderately similar to AF151841_1 CGI-83 protein [H.sapiens]	
3131 A		256	AA893032		ESTs	
3138 I		1047	AI178850		ESTs	
3143 J		540	AI010618		ESTs	
3143 E,H		1180	AI232408		ESTs	
3145 A		444	AA997237		EST	
3175 S		447	AA997414		ESTs	

TABLE 1

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
3189 A		448 AA997438				ESTs, Moderately similar to LDL receptor member LR2 [M. musculus]
3203 C		1624 NM_017039				Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
3207 A		449 AA997466				ESTs
3219 E		767 AI105065				ESTs, Highly similar to PNAD_MOUSE PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE [M. musculus]
3233 L		53 AA818105				ESTs, Moderately similar to Unknown gene product [H. sapiens]
3250 M		455 AA997765				Rattus norvegicus fibrillin-1 mRNA, complete cds
3253 F		1652 NM_017282				proteasome (prosome, macropain) proteasome (prosome, macropain)
3260 S		571 AI013875				ESTs, Moderate similarity to proteasome (prosome, macropain) subunit, alpha type 5
3266 L		915 AI171948				ESTs
3279 S		747 AI103224				ESTs, Weakly similar to putative short-chain dehydrogenase/reductase [R.norvegicus]
3280 C		1083 AI227699				ESTs
3292 M, N		1325 D00753				Rat mRNA for contrapain-like protease inhibitor related protein (CP1-26)
3365 A,B		518 AI008919				ESTs
3381 K		254 AA892993				ESTs
3418 A,C,D		936 AI175475				ESTs, Highly similar to NHPX_RAT NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG [R.norvegicus]
3430 J		1441 S85184				Cathepsin L

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title
3439 S		255 AA893000			ESTs, Highly similar to KIAA0564 protein [H.sapiens]	
3452 M N		452 AA997721			Rattus norvegicus orphan chemokine receptor mRNA, complete cds	
3486 H		869 A1170313			ESTs	
3504 A B		760 A104659			Rattus norvegicus mRNA for R-RCD1, complete cds	
3510 K		963 A1176423			ESTs, Highly similar to ZO1 MOUSE TIGHT JUNCTION PROTEIN ZO-1 [M.musculus]	
3513 S		1639 NM_017177	Glycerolipid metabolism	choline/ethanolamine kinase	choline/ethanolamine kinase Rat signal peptidase mRNA, complete cds	
3549 H I		1385 L11319			EST	
3558 S		463 AA998461			ESTs, Weakly similar to RET1_RAT RETINO-BINDING PROTEIN 1, CELLULAR [R.norvegicus]	
3570 O		464 AA998510			ESTs	
3587 J		1078 A1180253			Rattus norvegicus gene for hepatocarcinogenesis-related transcription factor (HTF), complete cds	
3617 N			1259 A1236021		ESTs, Weakly similar to JC1450 fibroblast growth factor receptor 4 - rat [R.norvegicus]	
3626 P			950 A1176031		ESTs, Highly similar to Opa-interacting protein Olp2 [H.sapiens]	
3631 S		302 AA924460			ESTs	
3660 B		467 AA998833				
3708 M		469 AA9989060				

TABLE 1

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GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title
3710 B,Q	470 AA989064				ESTs
3713 A,N	471 AA112571				ESTs
3720 S	471 AA989138				ESTs
3722 N	457 AA997979				ESTs
3730 N	460 AA989234				EST
				Rat mRNA for brain acyl-CoA synthetase II, complete cds	
3743 S	1335 D30666				EST
3749 P	461 AA989276				Uncoupling protein 2, mitochondrial
3776 Q	1679 NM_019354				Rattus norvegicus 250 kDa estrogen-specific protein mRNA, partial cds
3803 L,R	884 AA1170773				ESTs. Highly similar to PSD5, HUMAN 26S PROTEASOME SUBUNIT SSB [H.sapiens]
3816 J	1219 AI233729				ESTs. Weakly similar to nuclear RNA helicase [R.norvegicus]
3822 A	288 AA900863				ESTs. Weakly similar to nuclear RNA helicase [R.norvegicus]
3823 A	1196 AI233147				HMrATPase, H ⁺ transporting, lysosomal (vacuolar proton pump), beta isoform 2
3831 C,J	1525 Y12635		Oxidative phosphorylation	R.norvegicus mRNA for vacuolar adenosine triphosphatase subunit B	
3846 O	658 AI070895				ESTs. Weakly similar to similar to acyl-CoA dehydrogenases and epoxide hydrolases [C.elegans]
3849 A	567 AI013745				ESTs. Moderately similar to CGI-147 protein [H.sapiens]
3916 A,F	865 AI169947				ESTs
3917 B	1194 AI232970				ESTs
3929 O	270 AA894233				ESTs

TABLE 1

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GLGC ID	Nucleotide Sequence ID	GenBank Acc. ID	Pathways	Known Gene Name	Unigene Cluster Title
3934_A	544	AJ011510			ESTs
3959_A		292	AA901338		ESTs, Highly similar to IF2B_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT [H.sapiens]
3969_A		1001	AJ177055		ESTs
3972_Q		300	AA924307		ESTs
3976_E		61	AA818264		ESTs, Weakly similar to similar to GTPase-activating proteins [H.sapiens]
3981_A		554	AJ012235		ESTs
3995_A		545	AJ011678		ESTs
4017_A		63	AA818287		ESTs
4026_B,Q		1225	AJ233835		ESTs
4048_I		139	AA851814	Rattus norvegicus osteoactivin mRNA, complete cds	Rattus norvegicus osteoactivin mRNA, complete cds
4049_I		784	AJ112012		ESTs
4082_O		624	AJ045266		ESTs
4084_A		512	AJ008504		ESTs
4092_L		1095	AJ228723	Glycolysis, Gluconeogenesis	R.norvegicus phosphoglycerate mutase B, Isozyme (PGAM) mRNA, complete cds
4097_I		1037	AJ178635		ESTs
4119_J		720	AJ101901		ESTs
4127_H		1057	AJ179206		ESTs
4143_A		786	AJ112107		ESTs
4157_E		525	AJ009481		ESTs, Weakly similar to putative [C.elegans]
4168_E		527	AJ009654		ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
4178 I		170	AA859536		ESTs	
4179 A,C,E,R		1132	A1230431		ESTs	
4193 A,C,D,E,F,I		923	A1172274		ESTs, Weakly similar to l37195 AU-specific RNA-binding protein / enoyl-CoA hydrolase [H. sapiens]	
4199 G		1425	M83143	Sialyltransferase 1 (beta-Galactoside alpha 2,6-sialyltransferase)	Rat beta-galactoside-alpha 2,6-sialyltransferase mRNA	
4207 F		371	AA945591		ESTs, Weakly similar to JC5105 stromal cell-derived factor 2 - mouse [M.musculus]	
4224 G		1415	M31322		Rat sperm membrane protein (YWK-1) mRNA, 3' end	
4231 R		1159	A1231763		Rattus norvegicus late gestation lung 2 protein (Lg2) mRNA, complete cds	
4234 H		1665	NM_021577		Rattus norvegicus mRNA for AfC-1, complete cds	
4250 B		76	AA818700		ESTs	
4271 S		321	AA925603		ESTs, Moderately similar to AF153605, 1 androgen induced protein [H.sapiens]	
4272 S		1152	A1231309		ESTs, Moderately similar to AF153605, 1 androgen induced protein [H.sapiens]	
4281 A,G		1663	NM_019192	selenoprotein P, plasma, 1	selenoprotein P, plasma, 1	
4290 S		1323	AJ224120		Rattus norvegicus peroxisomal membrane protein Pmp26p (Peroxin-11)	
4291 A,H		79	AA818741		ESTs	

TABLE 1
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GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
4312 K		480 AB010635			Rattus norvegicus mRNA for carboxylesterase precursor, complete cds
4314 G,M		483 AF010597			Rattus norvegicus bile salt export pump (spgp) mRNA, complete cds
4318 F		474 AB005900			Rattus norvegicus mRNA for endothelial receptor for oxidized low-density lipoprotein, complete cds
4327 I		498 AF063447			Rattus norvegicus nuclear RNA helicase mRNA, complete cds
4330 A,C,D,E		80 AA818747			Rattus norvegicus stromal cell-derived factor-1 gamma mRNA, complete cds
4348 E		874 AI170447			Rattus norvegicus mRNA for norepinephrine transporter b (NETb), complete cds
4360 A		1356 H31813			ESTs
4371 E		295 AA924196			ESTs
4426 I		3 AA685974			ESTs
4438 S		2 AA684919			ESTs
4440 A,O		1189 AI232643			ESTs
4473 A		239 AA891965			ESTs
4504 Q		1725 NM_024159			Rattus norvegicus DOC-2 p59 isoform mRNA, complete cds
4520 O		751 AI103694	Oxidative phosphorylation, Ubiquinone biosynthesis	H3:NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)	Moderately similar to NADH-ubiquinone oxidoreductase subunit C- B8 [H.sapiens]
4553 A,C		999 AI177038			ESTs
4576 K		1049 AI178872			ESTs

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GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
4588 K		477 AB009636	1680 NM_019356		eukaryotic translation initiation factor 2, subunit 1 (alpha)	Rattus norvegicus mRNA for phosphoinositide 3-kinase, complete cds eukaryotic translation initiation factor 2, subunit 1 (alpha)
4592 C,D		1075 A1179991				ESTs
4610 E		718 A101582				ESTs
4650 G		1217 A1233714				ESTs
4670 A,N		279 AA898847				EST
4674 O						ESTs. Highly similar to IRF3_MOUSE_INTERFERON REGULATORY FACTOR 3 [Mus musculus]
4679 L		585 A1029847				ESTs
4719 A		1087 A1228285				ESTs
4725 L		282 AA900290				ESTs
4759 E		285 AA900553				ESTs
4781 C,D		1228 A1233925				ESTs
4856 I		752 A1103708				ESTs
4868 A		882 A1170763				ESTs
4892 P		611 A1044292				ESTs
4914 A		785 A1112086				ESTs
4929 E		296 AA924236				ESTs. Moderately similar to unknown [H.sapiens]
4931 S		297 AA924261				EST
4933 A,E,P		299 AA924301				ESTs
4937 A,L		1294 A1237189				Rattus norvegicus <i>rap7a</i> mRNA, complete cds
4940 S		1738 NM_022526				

TABLE 1

Document Number 1650775						
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
4944 A,F			301 AA924405		ESTs, Moderately similar to NOP56 HUMAN NUCLEOLAR PROTEIN	
4951 A		519 AI009026			NOP56 [H-sapiens]	ESTs
4952 C,J		86 AA818807			ESTs	
4969 M		795 AI113008			ESTs, Moderately similar to megakaryocyte stimulating factor [H-sapiens]	
5008 A,C		88 AA818821			ESTs	
5018 L		306 AA924767			ESTs	
5020 E		307 AA924768			ESTs, Weakly similar to MRJ [M.musculus]	
5027 A		308 AA9224793			ESTs	
5038 E		846 AI1692239			ESTs	
5046 A,L		1303 AI237855			ESTs	
5052 R		1270 AI236302			ESTs, Weakly similar to THRY RAT TRANSTHYRETIN PRECURSOR [R.norvegicus]	
5059 Q		1288 AI236947			ESTs	
5091 E		699 AI073092			ESTs	
5110 E,M		317 AA925274			ESTs	
5111 E		397 AA955729		Glycolysis/ Gluconeogenesis, Purine metabolism, Pyruvate metabolism	EST,ESTs	
5175 A		90 AA818895		Pyruvate kinase, muscle	Pyruvate kinase, muscle	ESTs
5219 A		322 AA925807				ESTs, Moderately similar to BcDNA, GH02974 [D.melanogaster]
5235 F		829 AI145569				

TABLE 1

Document Number 1650775						
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Names	Unigene Cluster Title
5291 M			1190 A1232700	Aminocyl-tRNA biosynthesis, Glutamate metabolism		ESTs, Moderately similar to SYQ_HUMAN GLUTAMYL-TRNA SYNTHETASE [H.sapiens]
5331 I		91	AA818986	Nicotinate and nicotinamide metabolism	HHs:glutaminyl-tRNA synthetase	ESTs, Weakly similar to PNMT
5339 E, M		911	A1171727	HMM:nicotinamide N-methyltransferase [R.norvegicus]		ESTs
5381 R		1038	AI178734			ESTs
5384 A,B,F		207	AA891041			ESTs
5434 E		1380	K01878	Propiomelanocortin, beta (endorphin, beta)	Rat proopiomelanocortin (POMC) gene	ESTs
5437 F		407	AA866810			ESTs
5461 A		613	AI044338			ESTs, Highly similar to AF172275_1
5464 B,O		614	A1044345			FUS2 [M.musculus]
5489 C,J		914	A1171795	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism	UDP-glucuronosyltransferase 1 family, member 1	ESTs, member 1
5492 G		1336	D38061	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism	UDP-glucuronosyltransferase 1 family, member 1	ESTs, member 1
5493 G,O		1433	S56936			

TABLE 1

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number: 1650775
5504 D		1165	A1231805			ESTs, Weakly similar to NUML_MOUSE NADH-UBIQUINONE OXIDOREDUCTASE MLQ SUBUNIT [M.musculus]	
5518 S		617	A1044550			EST	
5565 S		377	AA345879			ESTs, Weakly similar to mitochondrial very-long-chain acyl-CoA thioesterase [R.norvegicus]	
5602 S		1187	A1232611			ESTs	
5608 R		93	AA819041		Fibronectin 1	Fibronectin 1	
5616 M,S		1731	NM_019143		Fibronectin 1	Fibronectin 1	
5622 A		1731	NM_019143			ESTs	
5687 P		705	A101006			ESTs	
5696 L		621	A1045116			ESTs	
5733 C		1424	M81855	P-glycoprotein 2/ multidrug resistance 1b, P-glycoprotein/multidrug resistance 1	proteasome (prosome, macropain) subunit, alpha type 2	P-glycoprotein/multidrug resistance 1 ESTs, Moderately similar to DYNC_HUMAN DYNACTIN, 50 KD ISOFORM [H.sapiens]	
5740 L		680	A1072092		proteasome (prosome, macropain) subunit, alpha type 2	proteasome (prosome, macropain) subunit, alpha type 2	ESTs
5748 A		1650	NM_017279		proteasome (prosome, macropain) subunit, alpha type 2	ESTs, Weakly similar to DRAL [R.norvegicus]	
5749 A,H		1650	NM_017279			ESTs	
5754 L,R		133	AA850738				
5780 C,D				1019	A1177869		
5794 C				1212	A1233480		
5795 E				626	A1045441		

TABLE 1

Document Number: 1650775

GlGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
5813 A	1026	AJ178231			ESTs
5820 J	1285	AJ236771			ESTs
5824 K	627	AJ045555			EST
5863 A	95	AA819111			ESTs
5867 A,C,D	158	AA858953	Alanine and aspartate metabolism, Aminoacyl-tRNA biosynthesis	HiHs.asparaginyl-tRNA synthetase	ESTs, Highly similar to SYN_HUMAN ASPARAGINYL-TRNA SYNTHETASE, CYTOPLASMIC [H.sapiens] Rattus norvegicus mRNA for DORA protein
5885 I	1322	AJ223184			ESTs, Moderately similar to Vanin-1 [M.musculus]
5887 S	1063	AJ179099		vanin 1	ESTs
5899 A,D,F	867	AJ170038			ESTs
5920 G	843	AJ169163			ESTs
5923 A	65	AA818355			ESTs, Moderately similar to M phase phosphoprotein 10 [H.sapiens]
5926 C	1017	AJ177638			ESTs
5930 E	42	AA817688			ESTs
5932 J	756	AJ104254			ESTs, Highly similar to 2008147C protein RAkD [R.norvegicus]
5934 A,F	43	AA817695			ESTs
5937 J	908	AJ171684			ESTs
5943 A	1005	AJ177105			Rattus norvegicus amino acid transporter system A (ATA2) mRNA, complete cds
5953 H		893	AJ171231		ESTs
5966 H		89	AA818847		ESTs
5993 R		820	AJ144612		ESTs
5998 G		1317	AJ639501		ESTs
6003 E	54	AA818107			ESTs

TABLE 1

Document Number 1650775						
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc. ID	Pathways	Known Gene Name	Unigene Cluster Title
6007 A		55 AA818123				ESTs
6012 D		56 AA818139				ESTs
6013 N		1634 NM_017096			C-reactive protein	
6015 A,O		57 AA818158				ESTs
6016 A,C,D		58 AA818163				EST
6017 A		1676 NM_019292		carbonic anhydrase 3		
6018 E,N		96 AA819140		carbonic anhydrase 3		
6026 E		59 AA818211				EST
6032 E		60 AA818258				ESTs
6033 A		1195 AI233081				ESTs
6037 A		64 AA818288				ESTs
6039 D		330 AA942716			ESTs, Highly similar to HN1 [M.musculus]	
6060 A,O		77 AA818702				ESTs
6066 E		83 AA818781				ESTs
6072 A,B,E,F		1093 AI228630			ESTs, Weakly similar to Similarity to litosperm LEC14B protein [C.elegans]	
6085 C		916 AI171990			ESTs, Moderately similar to axonemal dynein heavy chain [H.sapiens]	
6101 R		881 AI170752				ESTs
6132 A,C,D		94 AA819055				EST
6143 A,C		771 AI105167			ESTs, Moderately similar to selenium- binding protein [H.sapiens]	
6151 G		98 AA819199				EST
6153 G		203 AA875531			Rattus norvegicus pro-alpha-2(I) collagen (col1az2), mRNA, complete cds	
6155 G		715 AI101443			Rattus norvegicus pro-alpha-2(I) collagen (col1az2), mRNA, complete cds	
6188 E		82 AA818774				ESTs

TABLE 1

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number 1650776
6189 B,E,G		1023	AJ178027			ESTs, Weakly similar to GTP_RAT GLUTATHIONE S-TRANSFERASE P [R.norvegicus]	
6190 A		107	AA819812			ESTs	
6193 I		1161	AJ1231797			ESTs	
6198 M		109	AA819840			ESTs	
6200 P		110	AA819853			ESTs, Highly similar to TNFC_MOUSE LYMPHOTOXIN-BETA [M.musculus]	
6213 N		726	AJ102190			ESTs	
6222 N		68	AA818474			ESTs	
6226 A		70	AA819821			ESTs	
6236 B,E,P		75	AA818627			ESTs, Moderately similar to ISII_RAT INSULIN-INDUCED PROTEIN 1 [R.norvegicus]	
6272 L				'		ESTs, Weakly similar to B39066 prolipherich protein 15 - rat [R.norvegicus]	
6291 H		875	AJ1170617			ESTs	
6292 S		822	AJ1144797			ESTs	
6295 N		422	AA864181			EST	
6321 A,J		103	AA819672			ESTs, Weakly similar to AIF-C1 [R.norvegicus]	
6322 A		712	AJ101256			EST	
6330 H		85	AA818801			ESTs	
		873	AJ1170426				
6366 A,E,H						Rattus norvegicus mRNA for signal peptidase 21kDa subunit, complete cds	
6380 A,C,D		152	AA858716			ESTs, Weakly similar to dJ413H6.1.1 [H.sapiens]	
		153	AA858758				

TABLE 1

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc. ID	Pathways	Known Gene Name	Unigene Cluster Title
6409 E		156	AAB58910			ESTs
6410 A		157	AAB58926			ESTs
6431 K,P		159	AAB59086			EST
6439 S		636	AI058436			ESTs
6440 R		160	AAB59130			ESTs
6443 A		161	AAB59150			ESTs
6473 A		1002	AJ177791			ESTs
6477 N		1371	J00735	Fibrinogen, gamma polypeptide	Fibrinogen, gamma polypeptide	
6479 K		860	AI169690	Fibrinogen, gamma polypeptide	Fibrinogen, gamma polypeptide	
6532 B,Q		1232	AI234105			
6533 E		155	AA858852		ESTs, Moderately similar to hypothetical protein (H.sapiens)	
6541 O		740	AJ102905			ESTs
					ESTs, Highly similar to S65755 tetrahydrofolylglutamate synthase [M.musculus]	
6549 O		949	AJ176002	Folate biosynthesis		
6553 S		594	AI030271			ESTs
6554 A		505	AF097723		Rattus norvegicus liver annexin-like protein (LAL) mRNA, complete cds	
6582 L		910	AJ171726			ESTs, Weakly similar to ESR1 RAT ESTROGEN RECEPTOR [R.norvegicus]
6585 F		1685	NM_022266		Rattus norvegicus mRNA for connective tissue growth factor, complete cds	
6604 A,O		1104	AI229192			ESTs

TABLE 1
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GlOG ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
6613 A,F				Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Tryptophan metabolism, Valine, leucine and isoleucine degradation	Rattus norvegicus L-3-hydroxyacyl-CoA dehydrogenase precursor (HAD) mRNA, complete cds; nuclear gene for mitochondrial product	Rattus norvegicus L-3-hydroxyacyl-CoA dehydrogenase precursor (HAD) mRNA, complete cds; nuclear gene for mitochondrial product
6615 A			335 AA942889		ESTs, Weakly similar to putative type III alcohol dehydrogenase [D.melanogaster]	ESTs
6632 A			1246 AI235277		ESTs	ESTs
6633 A,N			1098 AI228931		ESTs	ESTs
6640 A			716 AI101500		ESTs	ESTs
6667 K			905 AI171646		ESTs	ESTs
6673 E			612 AI044325		Rattus norvegicus mRNA for N-cadherin, complete cds	ESTs
6676 L			143 AA851967		ESTs	ESTs
6677 S			542 AI011471		ESTs	ESTs
6682 A			1168 AI232065		ESTs	ESTs
6686 R			952 AI176130		ESTs	ESTs
6761 A			513 AI008699		ESTs, Highly similar to methyl-CpG binding domain-containing protein MBD3 [M.musculus]	ESTs
6789 O,R			459 AA998207		ESTs	ESTs
6796 C			735 AI102753		ESTs	ESTs
6798 E			857 AI169619		ESTs	ESTs
6801 A,E,K			536 AI010316		ESTs	ESTs
6804 E			509 AI007877		ESTs	ESTs

TABLE 1

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc. ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number 1650775
6814 E		717	AI101534			EST_Rattus norvegicus Mdk mRNA for midkine, complete cds	
6820 A,D		1133	AI230439			ESTs	
6821 E,L		990	AI176841			ESTs	
6824 A,C,D,F,I		104	AA819709			ESTs	
6825 A,B,Q,S		631	AI045972			ESTs	
6855 A,L		899	AI171370			ESTs	
6861 H,R		995	AI176970			ESTs	
6879 I		907	AI171674			ESTs	
6892 J		33	AA800551	Pantothenate and CoA biosynthesis, Pyrimidine metabolism, beta-Alanine metabolism	Rattus norvegicus mRNA for dihydroxyuridine dehydrogenase, HTs:dihydroxyuridine dehydrogenase	(RD1) mRNA, complete cds	
6911 D		1343	DB5035			ESTs	
6919 N		537	AI010461			ESTs	
6975 O		953	AI176229			ESTs, Weakly similar to Dreg-2 protein [D.melanogaster]	
7003 A,L		593	AI030259			ESTs, Weakly similar to TERA_RAT TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE [R.nonvegicus]	
7036 C,J		1164	AI231801			ESTs	
7056 B,M		543	AI011503	Fructose and mannose metabolism, Glycolysis/ Gluconeogenesis, Pentose phosphate cycle	Aldolase A, fructose-bisphosphate		
7062 A		1533	NM_012495			Aldolase A, fructose-bisphosphate	

TABLE 1

GLGC ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number
7063 A,C,D	1533 NM_012495		Fructose and mannose metabolism, Glycolysis/ Gluconeogenesis, Pentose phosphate cycle	Aldolase A, fructose-biphosphate	Aldolase A, fructose-biphosphate	165075
7064 A,C	1533 NM_012495		Fructose and mannose metabolism, Glycolysis/ Gluconeogenesis, Pentose phosphate cycle	Aldolase A, fructose-biphosphate	Aldolase A, fructose-biphosphate	
7111 R	108 AA819816				ESTs	
7113 A	868 AA170260				ESTs	
7176 Q	809 AA137468				ESTs	
7161 C	1209 AA1233407				ESTs	
7176 Q	1306 AA1639029				ESTs	
7196 P	1585 NM_012904			Annexin 1 (p35) (Lipocortin 1)	ESTs	
7199 C,D	562 AA1013044			Annexin 1 (p35) (Lipocortin 1)	ESTs	
7225 M	564 AA1013657				ESTs	
7243 A,C	1218 AA1233717				ESTs	
7262 D,L	946 AA1175833				ESTs	
7271 C	1115 AA1228739				ESTs	
7295 S	572 AA1013876				ESTs	
7299 A	573 AA1013911				ESTs	
7301 J	111 AA819854				ESTs	
7352 A	577 AA1028973				ESTs, Weakly similar to AF165892_1	
7362 L	578 AA1029026				RNA-binding protein StaBP [R.norvegicus]	
7403 C,D	579 AA1029212				ESTs	

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GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title
7414 C,D	813 A1137586			ESTs; Highly similar to IMB3_HUMAN IMPORTIN BETA-3 SUBUNIT [H.sapiens]	
7420 S	580 A1029291			ESTs; Highly similar to ClpX-like protein [H.sapiens]	
7451 E,N	581 A1029450			ESTs; Moderately similar to SYEP_HUMAN MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [H.sapiens]	
7497 O	849 A1168302		Sphingophospholipid biosynthesis	HMsphingomyelin phosphodiesterase 1, acid lysosomal	
7517 S	582 A1029709				ESTs; Highly similar to AF115778_1 acid lysosomal [H.sapiens]
7528 H					ESTs; Highly similar to AF115778_1 short coiled coil protein SCOCO [M.musculus]
7531 A	749 A1103548				ESTs
7537 E	1298 A1237614				ESTs
7552 E,G,I	584 A1029829				EST
7582 A	629 A1045802				ESTs
7584 O	588 A1029996				ESTs
7586 L	601 A1043724				ESTs
7602 I	589 A1030024				Rattus norvegicus mRNA for of CBP-50 protein
7617 A	1320 A1001929				ESTs
7665 F	591 A1030170				ESTs
7681 A	596 A1030668				ESTs; Moderately similar to methyltransferase related protein [M.musculus]
	595 A1030449				

TABLE 1

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Krown Gene Name	Unigene Cluster Title	Document Number
7684_O		592	A10302422			ESTs	1650775
7690_I		1700	NM_022284			Rattus norvegicus uroguanylin mRNA, complete cds	
7697_A,M		992	A1176942			ESTs	
7743_P		651	A1070233			ESTs	
7784_A		1570	NM_012789	Dipeptidyl peptidase 4	Dipeptidyl peptidase 4	ESTs	
7785_A,C		1570	NM_012789	Dipeptidyl peptidase 4	Dipeptidyl peptidase 4	ESTs	
7806_J		67	AAB18421			EST	
7858_M,P		599	A1043654			ESTs	
7868_A		711	A1101229			ESTs	
7887_C,D		823	A1144832	Aminocetyl-tRNA biosynthesis,Arginine and proline metabolism	HHs:arginyl-tRNA synthetase	Moderately similar to SYR_HUMAN_ARGINYLYL-TRNA SYNTHETASE [H.sapiens]	
7888_A,C,D		1215	A1233583	Aminocetyl-tRNA biosynthesis,Arginine and proline metabolism	HHs:arginyl-tRNA synthetase	Moderately similar to SYR_HUMAN_ARGINYLYL-TRNA SYNTHETASE [H.sapiens]	
7892_F		1102	A1229172			ESTs, Weakly similar to FIBA_RAT FIBRINOGEN ALPH4/ALPHA-E CHAIN PRECURSOR [R.norvegicus]	
7893_A		604	A1043761			EST	
7903_A,E,F		605	A1043805			ESTs	
7916_E		606	A1043855	Sterol biosynthesis	HMM:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S.cerevisiae)	ESTs, Highly similar to sterol-C5-desaturase [M.musculus]	
7918_A		1069	A1179750			ESTs	
7927_A,H,O		831	A1145931	Aminosugars metabolism	HHs:UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase	R.norvegicus mRNA for UDP-N-acetyl-D-glucosamine-2-epimerase	

TABLE 1

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GLGC ID	Nucleotide Sequence ID	GenBank Acc-ID	Pathways	Known Gene Name	Unigene Cluster Title
7935 C	607 A1043945		Porphyrin and chlorophyll metabolism	HMM:ferrochelatase	ESTs
7936 A	202 AA875496				ESTs
7967 L	1124 A1230134		Purine metabolism	HHs:adenylate cyclase 9	ESTs
				EST, Weakly similar to putative integral membrane transport protein [R.norvegicus]	
8017 P	633 A1056341				ESTs
8053 I	932 A1175033				ESTs
8054 R	1089 A1228959				ESTs
8079 B,M,Q	637 A1056581				ESTs
8107 G	1318 A1639534			Protein tyrosine phosphatase, gamma (provisional HGMD symbol)	Moderately similar to PROP MOUSE PROPERDIN [M.musculus]
8124 E	742 A1103071				ESTs
				HMM:hemopoietic cell phosphatase	Rattus norvegicus protein-tyrosine phosphatase (SHP-1) mRNA, complete cds
8152 I	1478 U77038				ESTs
8173 E	450 AA897699				ESTs
8177 S	638 A1056603				ESTs
				Rat ferritin light chain subunit, mRNA, Rattus norvegicus kynurenone aminotransferase/glutamine transaminase K (Kat) gene, complete cds	
8215 L	909 A1171692				ESTs
8273 P	765 A1104908				
8274 B	641 A1059270				EST, Weakly similar to hypothetical protein [H.sapiens]
8310 P	1048 A1178868				ESTs

TABLE 1

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GLGC ID	Comparison Code	Nucleotide Sequence ID	Genbank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
8314 J		642	AI059396	Alanine and aspartate metabolism, Purine metabolism	HMr:adenylosuccinate synthetase 1, muscle	ESTs
8315 S		643	AI059389		HHs:microsomal glutathione S-transferase 3	ESTs, Highly similar to PUA1_MOUSE ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME [M.musculus]
8317 A,E		234	AA892234	Glutathione metabolism		ESTs, Moderately similar to microsomal glutathione S-transferase 3 [H.sapiens]
8356 G		645	AI059543			EST
8387 A		962	AI176365			ESTs
8477 A		1066	AI179167			ESTs
8515 N		127	AA849917			ESTs
8522 M,P		647	AI060071			ESTs
8549 A,F,H		1216	AI233639			ESTs
8592 G		1364	H33491		Rattus norvegicus sterol delta 8-isomerase (RSI) mRNA, complete cds	
8597 B,H		72	AA818593		Rattus norvegicus phosphatidate phosphohydrolase type 2 mRNA, complete cds	
8600 A		640	AI05956		ESTs	
8630 A		529	AI009677		ESTs	
8661 J		73	AA818604	Heat shock protein 70-1	Rattus norvegicus heat shock protein 70 (HS70) mRNA, complete cds	
8662 J		115	AA848563	Heat shock protein 70-1	Rattus norvegicus heat shock protein 70 (HS70) mRNA, complete cds	
8663 J		1527	Z27118	Heat shock protein 70-1	(HS70) mRNA, complete cds	

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GLDC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title
8664 J		1530	Z75029		Heat shock protein 70-1	ESTs, Rattus norvegicus heat shock protein 70 (HSP70) mRNA, complete cds
8665 J		675	A 071965		Heat shock protein 70-1	ESTs, Weakly similar to putative peroxisomal 2,4-dienoyl-CoA reductase [R.norvegicus]
8692 A		610	A 044247			ESTs
8700 E,M		634	A 058398			ESTs, Weakly similar to DnaJ homolog 2 [R.norvegicus]
8709 R		1185	A 232534			ESTs
8715 N		648	A 066920			ESTs
8728 R		74	A A818615			ESTs
8730 H		1028	A 178483			ESTs, Rattus norvegicus clone P22 unknown mRNA
8735 H		697	A 073047			ESTs, Weakly similar to thyroid hormone responsive protein [R,norvegicus]
8766 A		549	A 012085			ESTs
8820 S		650	A 070152			Nucleolin
8829 A		1567	NM_012749			ESTs
8864 P		652	A 070319			ESTs
8872 G,K		134	A A851050			ESTs
8880 A		824	A 144936			ESTs, Highly similar to Ki antigen [M.musculus]
8886 D		1221	A 233766			ESTs
8905 K		790	A 112511			ESTs
8928 I		212	A A891221			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
8946 A		656	AI070611			ESTs
8984 J		1735	NM_022539		Hsp:METHIONINE AMINOPEPTIDASE 2	Rattus norvegicus initiation factor 2 associated 67 kDa protein (p67) mRNA, complete cds
8993 R		948	AI175997			ESTs
9012 A		657	AI070879			EST
9015 K		1239	AI234810			ESTs
9016 A,B,C,D,E		659	AI070903			EST
9053 A		249	AA892861			ESTs
9063 A		1197	AI233162			ESTs
9072 G		942	AI175635			ESTs
9079 P		667	AI071251			ESTs
9128 L		903	AI171611			ESTs
9148 B		516	AI008813			ESTs
9164 H		1565	NM_012726			ESTs
9166 E		807	AI137466			ESTs
9170 E		983	AI176947			ESTs
9181 C,D		1071	AI179870			ESTs
9190 H		702	AI100835			ESTs
9191 A					EST, Weakly similar to PE2R_RAT 20-ALPHA-HYDROXYSTEROID DEHYDROGENASE [R.norvegicus]	
9192 E		681	AI072107			ESTs
		805	AI137345		Rat MHC class II RT1.B beta gene, encoding cell surface glycoprotein beta chain,Rat mRNA for MHC class II antigen RT1.B-1 beta-chain,Rattus norvegicus MHC class II antigen RT1.B beta chain mRNA, partial cds	
9223 Q		1417	M36151			

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Gl/Gc ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
9245 A		684	A 072278			ESTs
9267 Q		685	A 072384			ESTs, Moderately similar to human formiminotransferase cyclodeaminase [H.sapiens]
9326 A		799	A 136514			ESTs, Moderately similar to SPIN [H.sapiens]
9331 A,C,D		689	A 072633			ESTs
9336 A		691	A 072643			ESTs
9372 S		692	A 072712			ESTs
9373 S		802	A 136714			ESTs
9374 R		854	A 169557			ESTs, Highly similar to CDNG_MOUSE CYCLIN-DEPENDENT KINASE 6 INHIBITOR [M.musculus]
9399 A		693	A 072812			ESTs
9402 O,R		101	A A819383			ESTs
9423 S		1566	NM_012649			Ryudocan/syndecan 4
9424 N		1566	NM_012649			Ryudocan/syndecan 4
9425 A		27	A A800059			Ryudocan/syndecan 4
9432 E		695	A 072914			EST
9475 A,O		698	A 073059			ESTs
9486 L		69	A A818490			ESTs
9541 A		1704	NM_022542			Rat rhoB gene mRNA, complete cds
9572 R		660	A 071162			ESTs
9583 A		664	A 071185			ESTs
9595 B,E,Q		800	A I36630			ESTs
9598 E		1365	H33832			ESTs
9603 E		666	A 071227			Rat PRRHIS8 mRNA for ribosomal protein S8
9621 O		937	A 175486		ribosomal protein S7	

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
9627_A		840	AJ165041			ESTs
9635_N		676	AJ071987			ESTs, Weakly similar to Y281_HUMAN HYPOTHETICAL PROTEIN KIAA0281 [H.sapiens]
9668_K		669	AJ071538			ESTs
9674_L		1044	AJ178784			ESTs
9697_K		671	AJ071642			ESTs
9712_B,E		988	AJ178836			ESTs, Weakly similar to F25H5.6 [C.elegans]
9754_A		788	AJ112194			ESTs
9766_R		672	AJ071858			ESTs
9775_L		124	AA849767			Rattus norvegicus brain-enriched SH3-domain protein mRNA, complete cds
9784_C		710	AJ101226			ESTs
9796_C		677	AJ071990			Rattus norvegicus pEathy mRNA, complete cds
9800_R		678	AJ072014			ESTs, Weakly similar to AF165892_1 RNA-binding protein SiahBP [R.norvegicus]
9826_A,M		228	AA891950			ESTs
9889_A		618	AJ044621			EST
9905_A,G		221	AA891774			ESTs
9925_S		620	AJ044926			ESTs
9969_K		622	AJ045195			EST
9977_M		623	AJ045253			EST
10002_K		816	AJ137988			ESTs, Highly similar to myosin X [M.musculus]
10016_F,I		1673	NM_019289			Actin-related protein complex 1b
10019_J		1043	AJ178756			ESTs

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GLcc Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
10093 G	639 AJ058746	Ribosomal protein S5		Ribosomal protein S5	EST
10109 A	1562 X58465			Rattus norvegicus E-seplin long form mRNA, complete cds	ESTs
10176 A	102 AA819530				ESTs
10184 E	1363 H33426				ESTs
10187 E	985 AJ176781	Inhibitor of DNA binding 1, helix-loop-helix protein (splice variation)		Rattus norvegicus SERP1 mRNA, complete cds	ESTs
10200 L	644 AJ059444				ESTs
10248 A	1574 NM_012797				ESTs
10306 I	506 AF100470				ESTs, Moderately similar to CO5_HUMAN COMPLEMENT C5 PRECURSOR [H.sapiens]
10378 F	1205 AJ232300	Complement component 5			ESTs
10394 R	337 AA943564	Htr phosphoprotein, glycogen, liver (Hers disease, glycogen storage disease type VI)		R.norvegicus gene for glycogen phosphorylase (liver type)	
10509 A	1696 NM_022268	Starch and sucrose metabolism		ESTs, Highly similar to HG17_RAT NONHISTONE CHROMOSOMAL PROTEIN HMG-17 [R.norvegicus]	EST
10533 S	635 AJ058430				Rattus norvegicus outer mitochondrial membrane receptor rTOM20 mRNA, complete cds
10540 O	269 AA894027				Rattus norvegicus outer mitochondrial membrane receptor rTOM20 mRNA, complete cds
10544 A,B	1341 D63411				ESTs
10545 A	1455 U21871				
10549 C,D,E	39 AA801255				

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GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
10593 R	876	A1170673			ESTs, Highly similar to EST00098
10594 E	704	A1100878			ESTs, protein [H.sapiens]
10611 O	1018	A1177790			ESTs
10667 N	1273	A1236366		Rattus norvegicus RNA-binding protein	Rattus norvegicus mRNA, partial cds
10790 F.M	602	A1043728			EST
10879 A.N	687	A1072476			ESTs
10984 A.P	842	A1169156			ESTs, Weakly similar to HP33 [R.norvegicus]
11021 A.N	106	AA819767			ESTs
11039 G	1705	NM_022543			Rattus norvegicus steroid sensitive gene 1 protein (SSG-1) mRNA, complete cds
11048 E	668	A1071456			EST, Moderately similar to AF059166_1 EH domain-containing protein EHD1 [M.musculus]
11125 L	673	A1071867			ESTs, Highly similar to phosphatidylserine synthase-2 [M.musculus]
11127 E	674	A1071868			EST
11152 G	1629	NM_017073		Aminoacyl-tRNA biosynthesis, Arginine and proline metabolism, Glutamate metabolism, Nitrogen metabolism, Porphyrin and chlorophyll metabolism	Glutamine synthetase (glutamate-ammonia ligase)
					Glutamine synthetase (glutamate-ammonia ligase)

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GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
11153 G	1629	NM_017073	Aminocycl- tRNA biosynthesis, Arginine and proline metabolism, Glutamate metabolism, Nitrogen metabolism, Porphyrin and chlorophyll metabolism	Glutamine synthetase (glutamate-ammonia ligase)	Glutamine synthetase (glutamate-ammonia ligase)
11157 A,E	1184	A1232494			ESTs
11166 A	40	AA801346			ESTs, Highly similar to KIAA0315 [H.sapiens]
11172 P	338	AA943730			ESTs, Weakly similar to TISB_RAT
11174 E	333	AA942745			ESTs
11179 A,H	783	AI111559			ESTs
11205 A,G	919	AI172057			ESTs
11215 E	49	AA817921			ESTs, Moderately similar to weak similarity to <i>Arabidopsis thaliana</i> ubiquitin-like protein 8 [C.elegans]
11227 O	541	AI010660			ESTs
11228 A	739	AI102871			ESTs
11235 D	1068	AI179709			ESTs, Weakly similar to similar to C.elegans hypothetical protein CET01HB.1, CEC05C12.3, CEF54D1.5, similar to trp and trp-like proteins [H.sapiens]
11280 R	808	A1137420			ESTs, Moderately similar to imogen 44 [M.musculus]
11315 R	892	AI171229			

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TABLE 1							Document Number 1500775
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc. ID	Pathways	Known Gene Name	Unigene Cluster Title	
11322 E		526	AI009492			ESTs, Highly similar to Unigene [H.sapiens]	
11331 C		828	AI145556			ESTs	
11336 R		388	AA946441			ESTs	
11354 R		833	AI146215			ESTs	
11357 A		835	AI146237	Arginine and proline metabolism, Selenoamino acid metabolism, Urea cycle and metabolism of amino groups-beta-Alanine metabolism	HMM:spermidine synthase	ESTs, Highly similar to SPEE_MOUSE SPERMIDINE SYNTHASE [M.musculus]	
11403 A,D,L		889	AI171088	Arginine and proline metabolism, Selenoamino acid metabolism, Urea cycle and metabolism of amino groups-beta-Alanine metabolism	HMM:spermidine synthase	ESTs, Highly similar to SPEE_MOUSE SPERMIDINE SYNTHASE [M.musculus]	
11404 A,C,D,L		1291	AI237002			ESTs, Moderately similar to PTN3_HUMAN PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 3 [H.sapiens]	
11422 Q			26	AA799812		ESTs, Moderately similar to PTN3_HUMAN PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 3 [H.sapiens]	
11423 B,H,Q				26	AA799812		

TABLE 1

Gl/GC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigenes Cluster Title	Document Number 1650775
11426 H		896	A1171305			ESTs, Moderately similar to PTN3_HUMAN PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 3 [H_sapiens]	
11429 A,G		862	A1169706			ESTs	
11438 E		922	A1172189			ESTs, Moderately similar to 41BB_MOUSE 4-1BB LIGAND RECEPTOR PRECURSOR	
11465 O			1263	A1236084		[M_musculus]	
11483 J			487	AF020618		ESTs, Moderately similar to progression elevated gene 3 protein [R.norvegicus];Rattus norvegicus progression elevated gene 3 protein mRNA, complete cds	
11485 E		1248	A1235348			ESTs, Highly similar to nuclear transcriptional repressor Mph1 [M_musculus]	
11492 A		770	A1105145			ESTs	
11493 J		1356	H31287			ESTs, Weakly similar to putative serine/threonine protein kinase MAK-V [M_musculus]	
11494 J		1356	H31287			ESTs, Weakly similar to putative serine/threonine protein kinase MAK-V [M_musculus]	
11495 J		991	A1176901			ESTs, Weakly similar to putative serine/threonine protein kinase MAK-V [M_musculus]	
11504 A,B		906	A1171632			ESTs	

TABLE 1

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number: 1650775
11520 A			443 AA997063				ESTs, Weakly similar to CAG6_RAT
11527 A,C,R			1108 AI229307				CMP-N-ACETYLNEURAMINATE-BETA-1,4-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE [R.norvegicus]
11536 A			984 AI176739				ESTs
11561 C			1200 AI1233182				ESTs
11563 A			728 AI102560				ESTs
11576 A			832 AI146177				ESTs, Moderately similar to S65785_mel-
11590 E			78 AA818721				13a protein - mouse [M.musculus]
11596 M			665 AI071194				ESTs
11608 F			172 AA859633				ESTs
11619 L			701 AI100769				ESTs
11623 E			930 AI172471				ESTs, Highly similar to small EDRK-rich
11625 R			708 AI101167				factor 2 [M.musculus]
11635 A,G			173 AA859645				ESTs, Weakly similar to ARL5_RAT
11644 K,O			1247 AI235282				ADP-RIBOSYLATION FACTOR-LIKE
11645 F,M			725 AI102093				PROTEIN 5 [R.norvegicus]
11660 C,D			1050 AI178944				ESTs
11691 A,E			327 AA926193				Rattus norvegicus mRNA for
							Sulfotransfase K2

TABLE 1
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GLGC ID	Comparison Code	Nucleotide Sequence ID	Genbank Acc.[ID]	Pathways	Known Gene Name	Unigene Cluster Title
11693 A,C,D,E,K		836	A1168953			Rattus norvegicus mRNA for Sulfotransferase 1Z
11700 E		557	A1012574			ESTs
11720 B,O,Q		1174	A1232273			ESTs, Highly similar to RNA cyclase homolog [H.sapiens]
11731 P		736	A1102812			ESTs
11742 A,E		1544	NM_012961			Follistatin
11745 A		713	A1101262			ESTs
		475	AB006450	translocator of inner mitochondrial membrane 17 kDa, a		membrane 17 kDa, a
11821 O		653	A1070350			ESTs, Weakly similar to DP1_MOUSE POLYPOSIUS LOCUS PROTEIN 1 HOMOLOG [M.musculus]
11830 N		1052	A1179093			ESTs
11840 N		1526	Y15068			Rattus norvegicus mRNA for Hsp70/Hsp90 organizing protein
11850 G		1431	R46985			R.norvegicus mRNA for ribosomal protein L10a
11876 L		522	A1009321			ESTs
11893 B		1139	A1230951			ESTs
				Brain immunoglobulin like protein with tyrosine - based activation motifs, Protein tyrosine phosphatase, non-receptor type substrate 1 (SHP substrate 1)		Brain immunoglobulin like protein with tyrosine - based activation motifs, Protein tyrosine phosphatase, non-receptor type substrate 1 (SHP substrate 1)
11904 B,F,M,Q		1344	D85183			ESTs
11940 F,H		209	AA891108			ESTs
11959 A		217	AA891735			ESTs

TABLE 1 Document Number: 1650775

GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc. ID	Pathways	Known Gene Name	Unigene Cluster Title
11960 K		220 AA891740			ESTs, Weakly similar to EPOR_RAT ERYTHROPOIETIN RECEPTOR PRECURSOR [R.norvegicus]
11974 B		363 AA944953			ESTs
12058 R		1393 L25387	Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate cycle	Hsp6-PHOSPHOFRUCTOKINASE, TYPE C	ESTs, Highly similar to K6PP_RAT 6- PHOSPHOFRUCTOKINASE, TYPE C [R.norvegicus]
12064 A		32 AA800429			ESTs
12087 A		1683 NM_020082		ribonuclease 4	ESTs
12120 O		121 AA849365			
12155 K		1370 J00728	Fatty acid metabolism, Tryptophan metabolism, Fatty acid metabolism, Tryptophan metabolism	cytochrome P450, 2b19	cytochrome P450, 2b19
12156 B,G,K		1378 K00996	Fatty acid metabolism, Tryptophan metabolism	cytochrome P450, 2b19	cytochrome P450, 2b19
12157 K		1379 K01721	Fatty acid metabolism, Tryptophan metabolism	cytochrome P450, 2b19	cytochrome P450, 2b19
12158 K		1383 L00320	Fatty acid metabolism, Tryptophan metabolism	cytochrome P450, 2b19	cytochrome P450, 2b19
12160 A,K		66 AA818412	Tryptophan metabolism	cytochrome P450, 2b19	cytochrome P450, 2b19
12185 E		890 A1171094			ESTs, Weakly similar to Cys2/His2 zinc finger protein [R.norvegicus]
12198 R		273 AA899195			Rattus norvegicus replication factor C subunit 2 (RFC2) mRNA, partial cds
12203 L		274 AA899256			ESTs, Weakly similar to translation initiation factor [M.musculus]

TABLE 1

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GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
12215_E_S	696 AA072959				ESTs, Moderately similar to monoglyceride lipases [M.musculus]
12216_A	1106 AA1229240				ESTs
12217_M_P	342 AA943860				ESTs
12306_A_E_N	360 AA944888				ESTs
12312_A	263 AA8893453				ESTs
12314_G	372 AA945596				ESTs, Moderately similar to LECT2 precursor [H.sapiens]
12317_E_R	1237 AA1234361				ESTs
12331_A	389 AA946466				ESTs, Weakly similar to cytoplasmic aminopeptidase P [R.norvegicus]
12332_A	389 AA946466				ESTs, Weakly similar to cytoplasmic aminopeptidase P [R.norvegicus]
12361_O	433 AA965031				ESTs
12375_L	798 AA136478				ESTs, Highly similar to p116Rip [M.musculus]
12450_A_P	755 AA103956				ESTs, Weakly similar to predicted using Genefinder [C.elegans]
12463_Q	1191 AA1232706				ESTs
12467_S	1193 AA1232924				ESTs
12471_A	413 AA957433				ESTs
12551_I	1122 AA1230056				ESTs
12577_F_M	779 AA111344				Rattus norvegicus cyclin H mRNA, complete cds
12585_O	380 AA946034				ESTs, Highly similar to AF151803_1 CGI45 protein [H.sapiens]
12587_A	1120 AA1229979				ESTs
12613_I	1357 H31620				ESTs, Highly similar to hypothetical protein [H.sapiens]

TABLE 1

						Document Number 1690775
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
12614 C,D,R		933	AI175294		ESTs	
12825 R		458	AA988029		ESTs	
12855 A,O		1226	AI238836		ESTs	
12894 A		416	AA967906		ESTs	
					ESTs, Weakly similar to LIS1_MOUSE PLATELET ACTIVATING FACTOR ACETYLHYDROLASE IB ALPHA SUBUNIT [R.hornericus]	
12714 P		533	AI010050		ESTs	
12746 O		548	AI011809		ESTs	
12844 N		679	AI072054		ESTs	
12848 A,G		251	AA892916		ESTs, Weakly similar to hemomucin [D.melanogaster]	
12857 N		694	AI072866		ESTs	
12880 E		782	AI111558		ESTs	
12928 B,F,R		396	AA865564		ESTs	
12946 A,N		1088	AI229291		ESTs	
12956 L		1296	AI237580		ESTs	
12964 N		1267	AI236227		ESTs	
12965 C		792	AI112926		ESTs	
12969 J		794	AI112969		ESTs	
12999 C		956	AI176276	Aminosugars metabolism	ESTs	
13045 M		801	AI136702		ESTs	
13055 E		1054	AI1179100		ESTs, Highly similar to potential membrane protein C14orf1 [H.sapiens]	
13088 A,F,G		266	AA893495		ESTs, Highly similar to CBG_RAT CORTICOSTEROID-BINDING GLOBULIN PRECURSOR [R.hornericus]	

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
13092_O		1158	A1231547		HMM:FK506 binding protein 4 (59 kDa)	ESTs, Weakly similar to PPP5_RAT SERINE/THREONINE PROTEIN PHOSPHATASE 5 [R.norvegicus]
13093_B,O		552	A1012177		HMM:FK506 binding protein 4 (59 kDa)	ESTs, Weakly similar to PPP5_RAT SERINE/THREONINE PROTEIN PHOSPHATASE 5 [R.norvegicus]
13166_A,R		1039	A1178136			ESTs
13175_E		965	A1176465			ESTs
13203_A,C		1096	A1228128			ESTs
13229_O		154	AA858760			ESTs
13251_C,D,R		1059	A1179264			ESTs, Moderately similar to LZIP-1 and LZIP-2 [M.musculus]
13265_J		719	A1101708			ESTs
13283_A		1598	NM_013078	Arginine and proline metabolism, Urea cycle and metabolism of amino groups	Ornithine carbamoyltransferase	Ornithine carbamoyltransferase
13294_D		1220	A1233731			ESTs, Weakly similar to TCPA_RAT T-COMPLEX PROTEIN 1, ALPHA SUBUNIT [R.norvegicus]
13332_B,Q		257	AA839390			ESTs
13351_A,H		62	AA818271			ESTs
13353_M,N		938	A1175508			ESTs
13458_C,D,I		934	A1175338			ESTs
				Sphingoglycolipid metabolism	HHs:UDP-glucose ceramide glucosyltransferase	Rattus norvegicus UDP-glucose:ceramide glucosyltransferase
13467_C		817	A1138034			mRNA, complete cds
13501_R		957	A1176284			ESTs
13534_E		382	AA946187			ESTs

TABLE 1 Document Number 1650775

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title
13557	B,E,L,N	367	AA945090		ESTs	
13568	H	28	AA800169		ESTs	
13580	K	1030	AI178507		ESTs	
13581	E	1035	AI178602		ESTs	Highly similar to S26812
						transcription factor ATF-4 - mouse [M.musculus]
13634	A	1061	AI179381		ESTs	
13640	E,H	814	AI137761		ESTs	Highly similar to RL3_RAT 60S RIBOSOMAL PROTEIN L3 [R.norvegicus]
13646	C,D,E	1509	X62166			Rattus norvegicus serine protease gene, complete cds
13684	A,D,I	81	AA818770		ESTs	Rat alpha-crystallin B chain mRNA, complete cds
13723	D	1419	M55534	Crystallin, alpha polypeptide 2	ESTs	
13749	A	1089	AI228540		ESTs	
13757	A	1094	AI228676		ESTs	
13762	A,E	1129	AI230326		ESTs	
13799	L	947	AI175871		ESTs	
13812	R	1101	AI2289167		ESTs	
13838	R	1111	AI229416		ESTs	Weakly similar to KIAA0859 protein [H.sapiens]
13874	C,D	1117	AI229832		ESTs	
13895	M	1127	AI230270		ESTs	
13918	E	569	AI013832		ESTs	
13926	H	17	AA799601		ESTs	
13932	E,H,N	1142	AI230988		ESTs	

TABLE 1

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	
						ESTs, Moderately similar to SEC_HUMAN SEC PROTEIN [H.sapiens]	ESTs, Highly similar to DDX6_MOUSE PROBABLE ATP-DEPENDENT RNA HELICASE P54 [M.musculus]
13949 R		1149	A 231193			ESTs	
13963 A,O		1154	A 231388			ESTs	
13967 E		1155	A 231439			EST	
13992 Q		1281	A 236679			ESTs	
14007 A,E		1166	A 231808			ESTs	
14016 F		489	A 026505			ESTs	
14017 F		2111	AA891194	HHs:homogenitalis 1,2-dioxygenase (homogenitalic oxidase)		ESTs, Highly similar to homogenitalise 1,2-dioxygenase [M.musculus]	
14035 A		1177	A 232328	Tyrosine metabolism		ESTs, Weakly similar to PIR1 [H.sapiens]	
14051 A,C,D		1163	A 232489			ESTs	
14053 E		1243	A 235046			ESTs, Highly similar to AF073727_1	
14074 A		1206	A 233323			ESTs	
14081 P		1198	A 233164			ESTs	
14083 A		1009	A 177181			ESTs	
14095 A		1211	A 235468			ESTs	
14103 A		1199	A 233172			ESTs	
14116 S		1207	A 233361			ESTs	
14118 A		1208	A 233367			EST	

TABLE 1
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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
14126 E			1062 Al1793415		Rattus norvegicus tropomyosin non-muscle isoform NM1 (TPM-gamma) mRNA, complete cds; Rattus norvegicus tropomyosin non-muscle isoform NM3 (TPM-gamma) mRNA, complete cds	Rattus norvegicus tropomyosin non-muscle isoform NM1 (TPM-gamma)
14139 H			175 AA859700	Porphyrin and chlorophyll metabolism	HHs:neurotrophic tyrosine kinase, receptor, type 1	EST, Highly similar to PPOX_MOUSE [M.musculus]; EST, Moderately similar to PPOX_HUMAN PROTOPORPHYRINOGEN OXIDASE [H.sapiens]
14171 E			1024 Al178073			ESTs, Weakly similar to cDNA EST yk249b3.5 comes from this gene [C.elegans]
14181 A			1233 Al234107			ESTs
14185 P			177 AA859837	Purine metabolism	HMr:guanine deaminase	Rattus norvegicus guanine aminohydrolase (GAH) mRNA, complete cds
14195 E			775 Al105205			ESTs
14199 K			1234 Al234133			ESTs
14206 A			182 AA859894			ESTs
14208 A,B			723 Al102017			ESTs
14224 C			1140 Al230956			ESTs, Moderately similar to TFG protein [M.musculus]
14242 C,D			1086 Al228197			ESTs
14250 K			21 AA799729	Purine metabolism	Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)	ESTs, Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)

TABLE 1
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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title
14256 C		1118	AJ229902			ESTs
14264 S		1181	AJ232409			ESTs, Weakly similar to bK126B4.2 [H.sapiens]
14266 O		1366	H33842			ESTs, Highly similar to phosphoprotein [M.musculus]
14303 L		1148	AJ231159			ESTs, Highly similar to KIAA1049 protein [H.sapiens]
14312 A,E		1281	AJ236036			ESTs, Moderately similar to UBE-1b [M.musculus]
14330 P		233	AA892146			ESTs
14335 E		1006	AJ177115			ESTs
14355 A		171	AA659585			ESTs
14400 F,M		858	AJ169620			ESTs
14424 A,J		654	AJ070421			ESTs
14449 E		1235	AJ234152			ESTs
14458 C,I		826	AJ145095			ESTs
14462 C,D		703	AJ1000871			ESTs
14465 F		253	AA892950			ESTs, Moderately similar to mitochondrial DNA polymerase accessory subunit [M.musculus]
14491 M		535	AJ010147			ESTs
14504 M,P		25	AA799804			ESTs
14506 A		1359	H32584			ESTs, Highly similar to gp250 precursor [M.musculus]
14507 S		132	AA850618			ESTs
14512 A,G		793	AJ112964			ESTs
14584 A		1250	AJ235360			ESTs, Moderately similar to glutathione-S-transferase homolog [M.musculus]

TABLE 1
Document Number 1600775

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Act ID	Pathways	Known Gene Name	Unigene Cluster Title
14595 S		232 AA8892128			ESTs	
14600 E,R		38 AA801076			ESTs	
14619 C,D		1290 AI236989			ESTs	Moderately similar to Nilrin
14638 E		803 AI137049			[M.musculus]	
14693 A,C,D		1240 AI234830			ESTs, Weakly similar to ORF YKR081c [S.cerevisiae]	
14738 N,O		997 AI176993			ESTs	
14746 A		1252 AI235584			ESTs, Moderately similar to KIAA0922 protein [H.sapiens]	
14776 A,E,N		1256 AI235995			ESTs	
14840 K		1258 AI235950			ESTs	
14869 A		1301 AI237698			ESTs, Weakly similar to [prediction]	
14882 S		1264 AI236089		Esterase 2	Esterase 2	
14913 L,R		1324 D00362			ESTs	
		1274 AI236461			ESTs, Highly similar to lipoic acid synthetase [H.sapiens]	
14937 A,E		1293 AI237159			ESTs	
14939 C,D		1090 AI228557			ESTs	
14958 N		105 AA819744			ESTs	Rattus norvegicus Sprague Dawley protein kinase C receptor mRNA, complete cds
14959 I		1444 U03390			ESTs, Highly similar to integrase interactor 1a protein [M.musculus],Rattus norvegicus Sprague Dawley protein kinase C receptor mRNA, complete cds	
14960 A,G,O		897 AI171319				

TABLE 1
Document Number 1650775

GLGC .ID	Comparison Code	Nucleotide Sequence .ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
14962 A,C,D		845	A1169171			ESTs, Highly similar to ENHANCER OF RUDIMENTARY HOMOLOG [M.musculus]
14970 G,O		218	AA8891738	Sulfur metabolism	HH:sulfite oxidase	Rattus norvegicus sulfite oxidase mRNA, complete cds
14989 O		1012	A1177366		Integrin, beta 1	Integrin, non-specific ALP alkaline phosphatase
14996 A,N		1597	NM_013059	Folate biosynthesis, Glycerolipid metabolism	Tissue-non-specific ALP alkaline phosphatase	Tissue-non-specific ALP alkaline phosphatase
14997 A,E,N,O		1597	NM_013059	Folate biosynthesis, Glycerolipid metabolism	Tissue-non-specific ALP alkaline phosphatase	Rattus norvegicus tissue inhibitor of metalloproteinase-1 (TIMP1), mRNA, complete cds
15002 F		851	A1169327			Rattus norvegicus tissue inhibitor of metalloproteinase-1 (TIMP1), mRNA, complete cds
15003 F		851	A1169327			ESTs
15004 A		1244	A1235224			ESTs
15015 S		961	A1176363			ESTs
15016 A		928	A1172285			ESTs
15018 E,S		430	AA964688			ESTs
15029 A,C,D,E,P		878	A1170696			ESTs, Weakly similar to development-related protein [R.norvegicus]
15030 L		113	AA848378			ESTs
15032 A,D		1576	NM_012816	Methylacyl-CoA racemase alpha	Methylacyl-CoA racemase, alpha	ESTs, Highly similar to ATDA, MOUSE DIAMINE ACETYLTRANSFERASE [M.musculus]
15051 J,R		1271	A1236332	Arginine and proline metabolism	Spermidine / spermine N1-acetyltransferase (diamine acetyltransferase)	

TABLE 1

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GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
15055 A		1463 U48220	Fatty acid metabolism, Tryptophan metabolism	HHs: cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., - metabolizing) polypeptide 6	Rattus norvegicus cytochrome P450 2D18 mRNA, complete cds
15057 O		1675 NM_019291	Nitrogen metabolism	carbonic anhydrase 2	carbonic anhydrase 2
15070 H		1081 A1180442	Sterol biosynthesis	HHs:farnesyl diphosphate synthase (farnesy pyrophosphate synthetase, dimethylallyltransf erase, geranyltransf erase)	Rat testis-specific farnesy pyrophosphate synthetase mRNA, complete cds
15080 A		724 A1102045			ESTs, Highly similar to OS-4 protein [H.sapiens]
15089 F		530 A1009752			ESTs
15091 J		1040 A1178740		YY1 transcription factor	ESTs
15097 L,O		1548 NM_012588		Insulin-like growth factor-binding protein (IGF-BP3)	Insulin-like growth factor-binding protein (IGF-BP3)
15113 A,G		941 A1175590			ESTs, Highly similar to dj1118D24.1c [H.sapiens]
15116 P		190 AA874928			ESTs, Highly similar to sorting nexin 4 [H.sapiens]
15121 E		746 A1103159			Rattus norvegicus interferon-inducible protein 16 mRNA, complete cds
15122 E		1176 A1232303	Androgen and estrogen metabolism,Pentose and glucuronate interconversions,Porphyrin and chlorophyll metabolism,Starch and sucrose metabolism	UDP-glucuronosyltransferase 1 family, member 1	ESTs, Weakly similar to Sd1669p [M.musculus]
15127 B,K		1434 S56937			Rattus norvegicus UDP- glucuronosyltransferase (UGT1.1) gene, complete cds,Rattus norvegicus UDP- glucuronosyltransferase UG11A7 mRNA, complete cds, UDP- glucuronosyltransferase 1 family, member 1

TABLE 1
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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title
15135 A,D		1436	S71021		R.norvegicus mRNA for ribosomal protein L6	
15136 A		20	AA799672		R.norvegicus mRNA for ribosomal protein L6	
15139 H		818	A1144595		ESTs	
15141 E,F		1649	NM_017278	proteasome (prosome, macropain) subunit, alpha type 1	ESTs	
15149 R		164	AA859327		ESTs, Highly similar to KIAA0418	
15156 A,E		165	AA859341		[H.sapiens]	
15162 L		168	AA859350		ESTs	
15170 A,H,N		1299	A1237618		ESTs	
15171 J		1160	A1231792		ESTs, Moderately similar to BAG-family molecular chaperone regulator-3 [H.sapiens]	
15172 J		169	AA859362		ESTs, Moderately similar to BAG-family molecular chaperone regulator-3 [H.sapiens]	
15179 R		982	A1176675		ESTs	
15181 H		1245	A1235234		ESTs	
15189 M,N		1399	M11794	Metallothionein		
15190 N		729	A1102562	Metallothionein		
15191 N		964	A1176456	Metallothionein		
15197 A		778	A1105444		ESTs	
15203 I		1389	L19698	Rat GTP-binding protein (rat A) mRNA, complete cds		
15207 A,B,Q		147	AA858448		ESTs	
15239 A		1619	NM_016389	R.norvegicus (Sprague Dawley) ribosomal protein L15 mRNA		

TABLE 1

Document Number 1600776

GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
15240_A	609	A 044241			ESTs, Moderately similar to cell death activator CIDE-B [M.musculus]
15251_E,L	1011	A 177363			ESTs, Highly similar to CSK_RAT TYROSINE-PROTEIN KINASE CSK [R.norvegicus]
15281_I	1328	D 3623			ESTs
15282_D,I,L	1034	A 178573			ESTs
15283_D	148	AA 858548			ESTs
15291_J	780	A 111401	multiple inositol polyphosphate histidine phosphatase 1	multiple inositol polyphosphate histidine phosphatase 1	multiple inositol polyphosphate histidine phosphatase 1
15292_J	484	A 012714		FK506-binding protein 1 (12kD)	
15295_O	1602	NM_013102		B-cell translocation gene 2, anti-proliferative	FK506-binding protein 1 (12kD)
15299_A	1647	NM_017259		B-cell translocation gene 2, anti-proliferative	B-cell translocation gene 2, anti-proliferative
15300_A,F	1647	NM_017259		B-cell translocation gene 2, anti-proliferative	B-cell translocation gene 2, anti-proliferative
15301_A	1647	NM_017259		B-cell translocation gene 2, anti-proliferative	B-cell translocation gene 2, anti-proliferative
15312_C,D,I,J	198	AA 875126			ESTs
15313_C,D,J	198	AA 875126		calpastatin 1 heavy chain	ESTs
15315_G	1021	A 177911			
15345_L	902	A 177587		cofilin 1, non-muscle	
15365_D	1637	NM_017147			ESTs, Highly similar to IF39_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 [H.sapiens]
15374_C,D	1368	H 34186			[H.sapiens]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigenes Cluster Title
15382 A,J		926	AJ1172302		ESTs, Weakly similar to S43056 hypothetical protein - mouse [M.musculus]	
15391 K		534	AJ010083		Rat mRNA for HBP23 (heme-binding protein 23 kDa), complete cds	
15398 C		1277	AJ236568		ESTs	
15431 L		1641	NM_017187	high mobility group protein 2	high mobility group protein 2	
15441 K		834	AJ146216		EST	
15462 G		1447	U06230		Rattus norvegicus protein S mRNA, partial cds	
15467 H		1265	AJ236106		ESTs	
15480 F		201	AA875362		ESTs	
15490 J		1107	AJ229253		Rattus norvegicus zinc finger protein (pMLZ-4) mRNA, 3' untranslated region	
15491 H		979	AJ176642		ESTs	
15500 K		1110	AJ229337	procollagen C-proteinase enhancer	ESTs	
15503 P		1668	NM_019237	protein	procollagen C-proteinase enhancer	
15504 M,P		1668	NM_019237	procollagen C-proteinase enhancer	procollagen C-proteinase enhancer protein	
15519 A		1036	AJ178629	proteasome (prosome, macropain) subunit, beta type, 8 (low molecular mass polypeptide 7)	ESTs. Highly similar to PRCY_RAT PROTEASOME COMPONENT_C13 PRECURSOR [R.norvegicus]	
15534 O		955	AJ178266	proteasome (prosome, macropain)	ESTs	
15535 F		1653	NM_017283	subunit, alpha type 6	proteasome (prosome, macropain) subunit, alpha type 6	
15543 D,I		1163	AJ231800		ESTs	

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GLGC Comparison ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
15551 R		1138	A1230759			ESTs, Moderately similar to ornithine decarboxylase antizyme 2 [M.musculus]
15558 J		204	AAB75537			ESTs
15571 G		1413	M27207			R.norvegicus mRNA for collagen alpha1 procollagen, type I, alpha 1
15606 B,N		356	AA94401			ESTs
15612 A		1618	NM_0168987	Citrate cycle (TCA cycle)	ATP citrate lyase	ATP citrate lyase
15616 J		1562	NM_012699		Microvascular endothelial differentiation gene 1	Microvascular endothelial differentiation gene 1
15617 J		205	AA875620			ESTs
15634 H		1546	NM_012576		Glucocorticoid receptor	Glucocorticoid receptor
15642 A		1016	A1177503			R.norvegicus mRNA for histone H3.3
15645 K		879	A1170709			R.norvegicus mRNA for histone H3.3
15647 A,J		488	AF025424	Purine metabolism, Pyrimidine metabolism	HMrnRNA polymerase 1-2 (128 kDa subunit)	Rattus norvegicus RNA polymerase 1
15655 I,L		733	A1102739			127 kDa subunit mRNA, complete cds
15663 D,R		940	A1175566			ESTs
15672 S		281	AA900099			Rattus norvegicus mRNA for Tcfex-1, complete cds
15673 G		921	A1172107			Rat mRNA for 5E5 antigen, complete cds
15700 A,D		479	AB010466			Rat mRNA for 5E5 antigen, complete cds
15701 F,G		1645	NM_017220			Rattus norvegicus mRNA for multidrug resistance-associated protein (MRP)-like protein-1 (MLP-1), complete cds
						Rattus norvegicus mRNA for multidrug resistance-associated protein (MRP)-like protein-2 (MLP-2), complete cds

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GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
15755_A_K	1718 NM_022960			Rattus norvegicus neutral solute channel aquaporin 9 (AQP9) mRNA, complete cds	
15778_E	1726 NM_024163	575 AI013924		Rattus norvegicus brain-enriched guanylate kinase-associated protein 1 mRNA, complete cds	
15786_B_Q				ESTs	
15834_B_E	286 AA900580		Oxidative phosphorylation, Ubiquinone biosynthesis	HH:NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b)	ESTs, Moderately similar to NADH-ubiquinone oxidoreductase B14.5B subunit [H.sapiens]
15880_D	738 AI102868				ESTs, Weakly similar to phosphoserine aminotransferase [H.sapiens]
15881_C_D	738 AI102868				ESTs, Weakly similar to phosphoserine aminotransferase [H.sapiens]
15882_A_C_D	1126 AI230228	185 AA866216			ESTs, Weakly similar to phosphoserine aminotransferase [H.sapiens]
15884_A_Q					ESTs
15888_K	199 AA875225				Rat granine nucleotide-binding protein G i, alpha subunit mRNA, complete cds
15892_A_F	1074 AI179988				ESTs
15900_A_C_D	1202 AI233262				ESTs
15914_F	451 AA987711				ESTs
15933_A	200 AA875253				R.norvegicus ARL1 mRNA for ARF-like protein 1
15955_A_K_L	1175 AI232294				ESTs

TABLE 1

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number
15959 J	E,L	972	A1176540			ESTs	1650775
15961 P		550	A0172130			ESTs	
15980 H		186	AA866426			ESTs	
15987 K		187	AA866435			EST	
16006 A,F		497	AF062594		Rattus norvegicus nucleosome assembly protein mRNA, complete cds		
16023 G		225	AA891872	Nicotinate and nicotinamide metabolism	Nicotinamide nucleotide transhydrogenase [NAD(P)+ transhydrogenase]	ESTs, Highly similar to NAD(P)+ transhydrogenase [M.musculus]	
16053 I		1091	A1228596			ESTs, Weakly similar to weakly similar to gastrula zinc finger protein [C.elegans]	
16080 A,J,Q		1547	NM_012580	Porphyrin and chlorophyll metabolism	Heme oxygenase	Heme oxygenase	
16081 A,J,Q		1067	A1179610		Heme oxygenase	Heme oxygenase	
16085 A,C,D		189	AA874889			ESTs	
16087 L		1145	A1231011			ESTs	
16124 K		994	A1176953			ESTs, Weakly similar to melanocyte-specific gene 1 protein [R.norvegicus]	
16125 Q		503	AF090134			Rattus norvegicus ln-7-Ba mRNA, complete cds	
16134 A,H		265	AA893485			Rattus norvegicus clone BB.1.4.1 unknown Glu-Pro dipeptide repeat protein mRNA, complete cds	
16167 E		191	AA874941			ESTs, Moderately similar to adipophilin [H.sapiens]	

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GLGC ID	Comparison Code	Nucleotide Sequence- ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
16169 E		598	AJ030932		ESTs, Moderately similar to adipophilin [H.sapiens]	
16172 A		1179	AJ232341		ESTs, Weakly similar to C13B9.2 [C.elegans]	
16173 M,P		408	AA957003		Rattus norvegicus intercellular calcium- binding protein (MRPB) mRNA, complete cds	
16190 A,S		757	AJ104482		ESTs, Weakly similar to ECHM_RAT ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR [R.norvegicus]	
16205 L		1488	X06423		Rat mRNA for ribosomal protein SB	
16215 H		192	AA874999		ESTs, Moderately similar to AF13910.1 ARL-6 interacting protein-3 [M.musculus]	
16219 G		1557	NM_012656		Secreted acidic cysteine-rich glycoprotein (osteonectin)	Secreted acidic cysteine-rich glycoprotein (osteonectin)
16240 M		166	AA859342		ESTs, Moderately similar to DHB2_RAT ESTRADOL_17 BETA- DEHYDROGENASE 2 [R.norvegicus]	ESTs, Moderately similar to DHB2_RAT ESTRADOL_17 BETA- DEHYDROGENASE 2 [R.norvegicus]
16251 E,Q		347	AA944077	Solute carrier family 2 a 1 (facilitated glucose transporter) brain	Rat brain glucose-transporter protein mRNA, complete cds	Rat brain glucose-transporter protein mRNA, complete cds
16278 E,K		1338	D38381	Fatty acid metabolism, Tryptophan metabolism	Hsp.CYTOCHROME P450 3A18	R.norvegicus CYP3 mRNA
16283 O		1667	NM_019229	solute carrier family 12, member 4	solute carrier family 12, member 4	solute carrier family 12, member 4
16312 A		193	AAB75032		ESTs	ESTs
16314 A		167	AA859348		ESTs, Moderately similar to AF123655_1 FEZ1 [H.sapiens]	ESTs, Moderately similar to AF123655_1 FEZ1 [H.sapiens]
16317 B		194	AA875041			

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
16318 J		174	AA859648		ESTs, Weakly similar to Dnai homolog 2 [R.norvegicus]	
16319 K		195	AA875047		ESTs, Highly similar to TCPY_MOUSE_T COMPLEX PROTEIN 1, ZETA SUBUNIT [M.musculus]	
16321 C		1157	A1231506		ESTs	
16323 S		184	AA866240		EST	
16324 A		722	A1102009		ESTs	
16327 A,O		196	AA875050		ESTs, Weakly similar to choline/ethanolamine kinase [R.norvegicus]	
16361 H		1442	U01344	Hsp:ARYLAMINE N-ACETYLTRANSFERASE 1	Rattus norvegicus clone A-2 arylamine N-acetyltransferase mRNA, complete cds	
16364 A,H		235	AA892251		R.norvegicus mRNA for V1A arginine vasopressin receptor	
16366 P		250	AA892288		EST	
16367 P		250	AA892288		EST	
16408 F		145	AA852027		ESTs	
16409 S		145	AA852027		ESTs	
16438 I		958	A1176294		ESTs, Highly similar to SMND2_HUMAN SMALL NUCLEAR RIBONUCLEOPROTEIN SM D2 [H.sapiens]	
16446 A		214	AA891423		ESTs	
16449 H		1689	NM_019238	Sterol biosynthesis	farnesyl diphosphate farnesytransferase 1	
16458 B,Q		362	AA944956		ESTs	

TABLE 1

GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
16477_Q	983	A1176701			Rat low molecular weight fatty acid binding protein mRNA, complete cds
16513_C	118	AA848782			ESTs, Moderately similar to hypothetical protein [M.musculus]
16518_D					ESTs, Weakly similar to HS9B_RAT
16519_P	973	A1176546			HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus]
16524_H				Ceruloplasmin (ferroxidase)	Ceruloplasmin (ferroxidase)
16562_E_N					ESTs
16566_H					Rattus norvegicus d38 mitogen activated protein kinase mRNA, complete cds
16610_I					Rattus norvegicus mRNA for TIP1/20, complete cds
16616_R					Rattus norvegicus Y-box protein YB2 mRNA, complete cds
16618_C					ESTs
16623_E					Rattus norvegicus muscle Y-box protein ESTs
16649_I					ESTs
16650_I					Annexin V
16654_I					R.norvegicus mRNA for macrophage metalloelastase (MME)
16673_R					ESTs
16680_A					ESTs

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TABLE 1							Document Number: 1680775
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known_Gene Name	Unigene Cluster Title	
16683 I		1596 NM_013052		Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	
16684 I,O		1586 NM_013052	870 Al170327	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide			
16688 L							
16700 A,E,S		517 Al008838					
16701 A		517 Al008838					
16703 A,C,O		1030 Al179300					
16704 S		4 AA686132		Fructose and mannose metabolism	Hsp_KETOHEXOKINASE	Rat ketohexokinase mRNA, complete cds	
16726 A		1427 M86236					
16728 H		1020 Al177885					ESTs

GLGC Comparison ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
16730 A,I			23 AA799766			ESTs Moderately similar to JTV1_HUMAN JTV-1 PROTEIN [H.sapiens]
16747 L			336 AA943131			ESTs
16756 C,D			52 AA818089			ESTs, Highly similar to glycyl-tRNA synthetase [H.sapiens]
16765 A			632 AI0563319			ESTs
16766 A			632 AI072137			ESTs
				Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Propanoate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-alanine metabolism	HHs:hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (irrunctional protein), alpha subunit	Rat mRNA for mitochondrial long-chain enoyl-CoA hydrolase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit of mitochondrial trifunctional protein, complete cds
16768 N			1331 D16478			ESTs, Highly similar to glutathione transferase [R.norvegicus]
16780 E,K			1510 X62660			ESTs, Weakly similar to nonmuscle myosin heavy chain-A [R.norvegicus]
16783 L,O			553 AI012215			
				HSP-PROTEIN-TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 2	HSP-PROTEIN-TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 2	Rat PTP-S mRNA for protein-tyrosine phosphatase
16809 B,O,Q			1503 X58828			ESTs
16825 J			245 AA8928602			Rat alpha-2(I) promoter
16854 I			188 AA8666454			ESTs
16859 A,C,N			1283 AI236753			

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GL/GC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
16871_H	1583 NM_012887			Thymopoietin (lamina associated polypeptide 2)	Thymopoietin (lamina associated polypeptide 2)
16879_A.E.F	848 AI160284			ES1's	ES1's, Weakly similar to nitirase homolog 1 [M.musculus]
16883_A.C.D.I	446 AA997345		Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism	Rattus norvegicus 4-trimethylaminobutyraldehyde dehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme)	Rattus norvegicus 4-trimethylaminobutyraldehyde dehydrogenase (Tmabach) mRNA, complete cds
16884_B.E	754 AI103758		Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism	Rattus norvegicus 4-trimethylaminobutyraldehyde dehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme)	Rattus norvegicus 4-trimethylaminobutyraldehyde dehydrogenase (Tmabach) mRNA, complete cds
16885_A.B.E.Q	773 AI105188				

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
16894 O		144	AA852018		ESTs, Moderately similar to AF097362_1 gamma-interferon inducible lysosomal thiol reductase [H.sapiens]	
16944 S		320	AA825541		ESTs, Highly similar to protein L [M.musculus]	
16945 S		320	AA825541		ESTs, Highly similar to protein L [M.musculus]	
16847 E		1572	NM_0121793	Arginine and proline metabolism, Glycine, serine and threonine metabolism, Urea cycle and metabolism of amino groups	Guanyldioacetate methyltransferase	Guanyldioacetate methyltransferase
16958 G		92	AA819021		EST	EST
16961 P		1056	AI179236		ESTs	ESTs
16982 A		1608	NM_013144		Insulin-like growth factor binding protein 1	Insulin-like growth factor binding protein 1
16993 A		14	AA795960		ESTs	ESTs
17027 A,E				Galactose metabolism, Nucleotide sugars metabolism, Pentose and glucuronate interconversions, Starch and sucrose metabolism	HHs: UDP-glucose pyrophosphorylase 2	ESTs, Highly similar to UDP1_HUMAN UTP-GLUCOSE-1-PHOSPHATE URIDYLYL TRANSFERASE 1 [H.sapiens]
17049 A		929	AI172417	Prostaglandin and leukotriene metabolism		ESTs, Weakly similar to B.subtilis YQUC protein [C.elegans]
17064 I		1660	NM_019170	carbonyl reductase		carbonyl reductase

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
17090	G.K		1474 U73174	Glutamate metabolism, Glutathione metabolism	HHs:glutathione reductase	Rattus norvegicus glutathione reductase mRNA, complete cds
17091	G.K		1474 U73174	Glutathione metabolism	HHs:glutathione reductase	Rattus norvegicus glutathione reductase mRNA, complete cds
17092	K		259 AA893189	Glutamate metabolism, Glutathione metabolism	HHs:glutathione reductase	Rattus norvegicus glutathione reductase mRNA, complete cds
17107	E		1638 NM_017160		ribosomal protein S6	ribosomal protein S6
17117	K		1085 AI228042			ESTs, Weakly similar to AC007080_2 NG38 [M.musculus]
17154	A		1407 M15683			Rat clathrin light chain (LCB2) mRNA, complete cds. Rat clathrin light chain (LCB3) mRNA, complete cds
17157	I		326 AA9296129			ESTs, Highly similar to AF168795_1 schlafen-4 [R.norvegicus]
17158	H		1699 NM_022298			Rat mRNA encoding alpha-tubulin ESTs
17167	M		566 A1013690			R.norvegicus AS1 mRNA for mammalian equivalent of bacterial large ribosomal subunit protein L22
17175	A		1501 X58389			ESTs, Highly similar to eif3 p66 [M.musculus]
17225	A,I		215 AA891553			ESTs, Weakly similar to p60 protein [R.norvegicus]
17256	A		219 AA891739			Cyclin D3
17257	E,R		1568 NM_012766			Cyclin D3
17258	P		1568 NM_012766			Cyclin D3
17261	R		1568 NM_012766			Cyclin D3
17277	B,P,Q		523 A1009338			Rattus norvegicus glycine-, glutamate-, thiencyclohexylphosphidine-binding protein mRNA, complete cds

TABLE 1

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title
17281 M,P		1450	U10697	Hsp;LIVER CARBOXYLESTERASE 4 PRECURSOR	R.norvegicus mRNA for pi esterase (ES-4)	
17291 E		931	A1172491	HHS:isocitrate dehydrogenase 2 (NADP+), mitochondrial	ESTs, Weakly similar to IDHC_RAT ISOCITRATE DEHYDROGENASE [R.norvegicus]	
17324 A		1686	NM_021593		Rattus norvegicus kynurenic 3-hydroxylase mRNA, complete cds	
17334 A		151	AA858704		ESTs, Highly similar to responsible for hereditary multiple exostosis [M.musculus]	
17335 A		732	A1102634		ESTs, Weakly similar to W06B4.2 [C.elegans]	
17337 J		472	AB0007117	Methionine metabolism, Selenoamino acid metabolism	HHS:methionine adenosyltransferase II, alpha	
17339 A		123	AA849497		ESTs	
17340 A,E		507	A1007803		Rattus norvegicus ERM-binding phosphoprotein mRNA, complete cds	
17368 E,R		284	AA900548		ESTs	
17369 C,I,P		812	A1137572		ESTs	
17377 A		1491	X13058	Tumor protein p53 (Li-Fraumeni syndrome)	Rat mRNA for nuclear oncoprotein p53	
17393 A,O		1377	J04943	Nucleoplasmin-related protein (Nuclear protein B23)	Nucleoplasmin-related protein (Nuclear protein B23)	
17400 E		744	A1103097		ESTs, Highly similar to ATPK_MOUSE ATP SYNTHASE F CHAIN, MITOCHONDRIAL [M.musculus]	
17401 A		1595	NM_013043	Transforming growth factor beta stimulated clone 22	Transforming growth factor beta stimulated clone 22	

TABLE 1

GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
17451 E		806 A137356			ESTs, Highly similar to DHYS_HUMAN DEOXYHYDROUSINE SYNTHASE [H.sapiens]
17479 R		827 A145385			ESTs
17481 E		1529 Z49761			R.norvegicus mRNA for RT1-Ma
17496 A		325 AA926109			ESTs
17500 I,P		1713 NM_022866			Rattus norvegicus sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
17506 L		649 A1070068			ESTs
17516 O	1739 NM_017321		iron-responsive element-binding protein	iron-responsive element-binding protein	
17524 A	539 A10568				ESTs
17541 G,K	1580 NM_012844		Epoxye hydrolase 1 (microsomal xenobiotic hydrolase)	Epoxye hydrolase 1 (microsomal xenobiotic hydrolase),	
17571 H,I	1276 A1236484			Rattus norvegicus mRNA for hnRNP protein, partial	
17572 E	71 AA818524			Rattus norvegicus mRNA for hnRNP protein, partial	
17589 A	248 AA892851			ESTs	
17590 F	248 AA892851			ESTs	
17591 A	888 A1717354			ESTs	
17613 O	10 AA799511			ESTs	
17617 E		1269 A1236301		ESTs, Weakly similar to FKB1_RAT FK506-BINDING PROTEIN [R.norvegicus]	
17644 R		293 AA824036		ESTs	
17664 B,Q		1238 A1234496		ESTs	

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc. ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number 1650776
17672 N		1123	AJ230074	Oxidative phosphorylation, Ubiquinone biosynthesis	HMM:NADH ubiquinone oxidoreductase subunit MWFE	ESTs, Highly similar to NIMM_MOUSE NADH-UBIQUINONE OXIDOREDUCTASE MWFE SUBUNIT [M.musculus]	
17677 E		683	AJ072246			ESTs	
17683 N		700	AJ073257			ESTs	
17684 G		236	AA892345			Rat mRNA for dimethyl/glycine dehydrogenase (EC number 1.5.99.2)	
17685 K		797	AJ113055			EST	
17687 C		12	AA799531			ESTs, Weakly similar to predicted using GeneFinder [C.elegans]	
17688 A		12	AA799531			ESTs, Weakly similar to predicted using GeneFinder [C.elegans]	
17695 N				*		ESTs, Weakly similar to putative peroxisomal 2,4-dienoyl-CoA reductase [R.norvegicus]	
17699 O		135	AA851233			ESTs, Weakly similar to NG28	
17709 A		1456	U24469		Tenascin X	[M.musculus]	
17730 G		1709	NM_022697			Tenacin X	
17734 C,D						Rat mRNA for ribosomal protein L28	
17735 C,D		466	AA998683			ESTs,Rattus norvegicus heat shock protein 27 (hsp 27) gene, complete cds	
17736 C,D		981	AJ176658			ESTs,Rattus norvegicus heat shock protein 27 (hsp 27) gene, complete cds	
17747 E		1428	M86389			ESTs,Rattus norvegicus heat shock protein 27 (hsp 27) gene, complete cds	
		1236	AJ234223			ESTs, Highly similar to cellular apoptosis susceptibility protein [H.sapiens]	

TABLE 1

GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number 1630775
17753 J	748	A1103246			ESTs, Highly similar to S65588 CCAAT-binding factor CBF2 - mouse [M.musculus]	
17754 I	261	AA8833246			ESTs, Highly similar to vacuolar H ⁺ -ATPase subunit D [H.sapiens]	
17758 G	1645	NM_017220	Butanate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Propanoate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-alanine metabolism	HTs.enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	Rat peroxisomal enoyl-CoA: hydratase-3-hydroxyacyl-CoA bifunctional enzyme mRNA, complete cds	
17768 B	774	A105196			ESTs	
17785 N	1534	NM_012501		Apolipoprotein C-III	Apolipoprotein C-II	
17788 K	271	AA889045		Esterase Diformylglutathione hydrolase	ESTs, Highly similar to sid478p [M.musculus]	
17794 E_N	772	A105184	Cyanoamino acid metabolism,Glycine, serine and threonine metabolism,Lysine degradation,Methane metabolism,One carbon pool by folate	HTs:serine hydroxymethyltransferase 1 (soluble)	ESTs	
17800 N	262	AA8893436			ESTs	
17809 B	5	AA686461			Rat ribosomal protein L30 mRNA, complete cds	

Document Number 1650775

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
17812 A,E		841	A1169076	Glutathione metabolism, Tyrosine metabolism	Hm/glutathione transferase zeta 1 (maleylacetooacetate isomerase)	ESTs
17819 A		891	A1171096			ESTs, Highly similar to unknown [H.sapiens]
17844 A,E		398	AA955927			ESTs
17847 A		1025	A1178214			ESTs, Weakly similar to TCPA, RAT-T-COMPLEX PROTEIN 1, ALPHA SUBUNIT [R.norvegicus]
17850 A		734	A1102750			Rat mRNA for MRC OX-45 surface antigen
17854 Q		1490 X13016			Selenoprotein W muscle 1	Selenoprotein W muscle 1
17884 E,F		1594 NM_013027			Interferon-related developmental regulator 1	Interferon-related developmental regulator 1
17908 A,J		1670 NM_019242				Rat/t nonneuritic membrane interacting protein of RGS16 (Mir 6) mRNA, complete cds
17935 S		289	AA901006			ESTs
17950 Q		1278	A1236590			ESTs
17955 L		590	A1030069			ESTs
17956 I		427	AA964379		adaptor-related protein complex AP-1, beta 1 subunit	adaptor-related protein complex AP-1, beta 1 subunit
17982 A		1727	NM_017010		Glutamate receptor, ionotropic, N-methyl D-aspartate 1;Rat N-methyl-D-aspartate receptor (NMDARI) gene, first exon	Glutamate receptor, ionotropic, N-methyl D-aspartate 1;Rat N-methyl-D-aspartate receptor (NMDARI) gene, first exon

TABLE 1

GI/GC Comparison ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number: 165075
18001 A		149	AA858573			ESTs, Highly similar to SP24 - RAT SECRETED PHOSPHOPROTEIN 24 [R.norvegicus] Rattus norvegicus spp-24 precursor mRNA, partial cds	
18002 ADE			600	AI043655		ESTs, Highly similar to SP24 - RAT SECRETED PHOSPHOPROTEIN 24 [R.norvegicus] Rattus norvegicus spp-24 precursor mRNA, partial cds	
18028 G		1337	D38062			Rattus norvegicus UGP-glucuronosyltransferase UGT1A7 mRNA, complete cds	
18029 S		1418	M38759			Sex hormone binding globulin or androgen-binding protein	
18043 J		487	AF020618			Rattus norvegicus progression elevated gene 3 protein mRNA, complete cds	
18046 I			500	AF072892		Rattus norvegicus versican V0 isoform mRNA, partial cds, Rattus norvegicus versican V3 isoform precursor, mRNA, complete cds	
18082 S		478	AB010429			R.norvegicus mRNA for mitochondrial very-long-chain acyl-CoA thioesterase	
18083 S		1524	Y09333			Hsp ACYL COENZYME A THIOESTER HYDROLASE, MITOCHONDRIAL PRECURSOR	R.norvegicus mRNA for mitochondrial very-long-chain acyl-CoA thioesterase
18099 G			1604	NM_013119		ESTs, Highly similar to AF0054 sodium channel protein IIIb, long form - rat [R.norvegicus]	
18107 I		1717	NM_022949			R.norvegicus mRNA for ribosomal protein L14	

TABLE 1
Document Number 1650775

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc. ID	Pathways	Known Gene Name	Unigene Cluster Title
18109 A		1577 NM_012823			Annexin III (Lipocortin III)	ESTs, Weakly similar to LUR13 annexin III - rat [R.norvegicus]
18115 A		31 AA800339				ESTs
18125 S		515 AJ008787				ESTs
18136 H		737 AJ102820				ESTs
18141 O		1014 AJ177413		ATP synthase subunit d	ATP synthase subunit d,ESTs, Weakly similar to myo-inositol-1-phosphate synthase [D.melanogaster]	ESTs, Highly similar to ACDV_RAT_ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR [R.norvegicus]
18203 P		1584 NM_012891				ESTs, Highly similar to CDC45L
18235 L		758 AJ104523				ESTs, Highly similar to CDC45L [M.musculus]
18237 Q		1065 AJ179539				ESTs
18259 J		1280 AJ236601				ESTs, Moderately similar to KIAA0740 protein [H.sapiens]
18272 B		6 AA799294				ESTs, Highly similar to Ring3 [M.musculus]
18280 L		384 AAQ46361				ESTs
18285 R		341 AAQ45791				Rattus norvegicus FAT mRNA, complete cds
18316 K		499 AF072411				Rattus norvegicus FAT mRNA, complete cds
18348 S		385 AAQ46368				ESTs
18323 E		556 AJ012498				ESTs
18349 J		22 AA799744				ESTs

TABLE 1

GLGC ID.	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number: 1650775
18369 G		19	AA799645			Ratius norvegicus phospholemman chloride channel mRNA, complete cds	
18389 A,B,Q		9	AA799498		Brain natriuretic factor	Ratius norvegicus brain natriuretic peptide (BNP) mRNA, complete cds	
18390 A,E		128	AA850038			ESTs	
18418 C		969	A1176483			ESTs	
18452 A		1630	NM_017074	Cysteine metabolism, Methionine metabolism, Nitrogen metabolism, Selenoamino acid metabolism	CTL target antigen	CTL target antigen	
18453 A			1630 NM_017074	Methionine metabolism, Nitrogen metabolism, Selenoamino acid metabolism	CTL target antigen	CTL target antigen	
18465 B,Q		1077	A1180187			ESTs	
18473 K		838	A1168975			ESTs	
18482 H		1311	A1639151			ESTs, Highly similar to pinin [H.sapiens]	
18484 L		1249	A1235349			ESTs, Highly similar to KIAA0184 [H.sapiens]	
18495 B		1307	A1639042			ESTs	
18501 J		1414	M31178			Rat calbindin D28 mRNA, complete cds	
18522 A,E		830	A1145870			ESTs	
18529 B,Q		1136	A1230716			ESTs	
18580 M,P		142	AA851963			ESTs	
18584 H		216	AA891694			ESTs	

TABLE 1

Document ID Number 1650775					
GLGC Comparison ID	Nucleotide Sequence ID	GenBank AccID	Pathways	Known Gene Name	Unigene Cluster Title
18588 E	276 AA899635		Nucleotide sugars metabolism, Pentose and glucuronate interconversions, Starch and sucrose metabolism		ESTs, Moderately similar to 2020265A BRG1 protein [M.musculus]
18597 A	481 AB013732		HMM: UDP-glucose dehydrogenase		Rattus norvegicus mRNA for UDP-Glucose dehydrogenase, complete cds
18604 N	1292 AI237124				ESTs
18606 A	1497 K53504				ESTs, Highly similar to RL12_RAT 60S RIBOSOMAL PROTEIN L12 [R.norvegicus]
18612 EO	1092 AI228624				ESTs, Highly similar to RL23_HUMAN 60S RIBOSOMAL PROTEIN L23 [R.norvegicus]
18647 E	1435 SG893167				ESTs, Weakly similar to HS9B_RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus]
18660 A	894 AI171262		cyclin G2		ESTs
18661 A	376 AA945751				
18685 L	453 AA997746		dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	
18705 I	1732 NM_020103	Fatty acid metabolism	Ly6-C antigen gene	Ly6-C antigen gene	
18727 S	1685 NM_021577	Alanine and aspartate metabolism,Arginine and proline metabolism,Urea cycle and metabolism of amino groups			Rat mRNA for argininosuccinate lyase, complete cds

TABLE 1

Gene ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number 1650775
18742 O_S		769 Al105131				ESTs, Highly similar to AF189764_1	
18746 S		900 Al171506		Pyruvate metabolism	Malic enzyme 1, soluble	alpha/beta hydrolase-1 [M.musculus]	
18747 S		1550 NM_012600		Pyruvate metabolism	Malic enzyme 1, soluble	Malic enzyme 1, soluble	
18749 S		1550 NM_012600		Pyruvate metabolism	Malic enzyme 1, soluble	Malic enzyme 1, soluble	
18755 C_D		1279 Al236589				ESTs	
18783 N		1282 Al236746				ESTs	
18792 A		662 Al071177				ESTs	
18795 N		1483 U95001				ESTs	
18796 A		45 AA817761				ESTs	
18829 H		84 AA818796				ESTs, Moderately similar to PLTP_MOUSE PHOSPHOLIPID TRANSFER PROTEIN PRECURSOR [M.musculus]	
18837 G		901 Al171583				ESTs, Weakly similar to N-copine [M.musculus]	
18854 A		1300 Al237636				Rattus norvegicus mRNA for hydroxysteroid sulfotransferase subunit, complete cds	
18860 A_K		861 Al168695		Androgen and estrogen metabolism, Sulfur metabolism	Hsp/ALCOHOL SULFOTRANSFERASE	Rattus norvegicus mRNA for hydroxysteroid sulfotransferase subunit, complete cds	
18861 A		1329 D14989				Rattus norvegicus mRNA for serine protease, complete cds	
18867 A		1348 D88250				ESTs	
18877 O		666 Al072383				ESTs, Highly similar to AF157028_1	
18885 R		583 Al029827				protein phosphatase 1 methylesterase-1 [H.sapiens]	

TABLE 1

Document Number 1650775						
GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	
18886 R		340 AA943785			ESTs, ESTs, Highly similar to AF-157028_1 protein phosphatase methylesterase-1 [H.sapiens]	
18890 B,P,S		280 AA899644			ESTs	
18891 B,Q,S		303 AA524593			ESTs	
18900 F		1214 A1233570	Oxidative phosphorylation, Ubiquinone biosynthesis	HHs:NADH dehydrogenase (ubiquinone) Fe-S protein 2 (49kD) (NADH-coenzyme Q reductase)	ESTs, Highly similar to PSD8_HUMAN 26S PROTEASOME REGULATORY SUBUNIT S14 [H.sapiens]	
18905 E		883 A1170770			ESTs, Highly similar to NADH-ubiquinone oxidoreductase NDUF52 subunit [H.sapiens]	
18906 A,K		243 AA892561			ESTs, Moderately similar to PTD012 [H.sapiens]	
18908 A		122 AA849426			ESTs	
18909 A		122 AA849426			ESTs	
18910 A		1182 A1232419			ESTs	
			Bile acid biosynthesis, Butanate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Synthesis and degradation of ketone bodies,			
18956 S		1631 NM_017075	Tryptophan metabolism	Acetyl-Co A acetyltransferase 1, mitochondrial	Acetyl-Co A acetyltransferase 1, mitochondrial	
18960 A		1004 A1177103			ESTs	

TABLE 1

Document Number 1630775						
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
18962 R		574	AJ013918		Rattus norvegicus TM6P1 [TM6P1]	mRNA, complete cds
18974 M		319	AA925384		ESTs	Moderately similar to hnRNP protein [R.norvegicus]
18981 H		11	AA799523		Glutathione-S-transferase, alpha type (Yc?)	Glutathione-S-transferase, alpha type (Yc?)
18990 G		1438	ST7506	Glutathione metabolism	ESTs	
18996 N		1027	AJ178326		ESTs	
19012 J,K		918	AJ172056		ESTs	Rat S-100 related protein mRNA, complete cds, clone 42C
19040 I		1374	J03627		ESTs	Highly similar to methyl-CpG binding protein MBD2 [M.musculus]
19043 F		130	AA850378		ESTs	Highly similar to methyl-CpG binding protein MBD2 [M.musculus]
19044 S		386	AA946379		ESTs	
19052 E,R		1253	AJ235675		ESTs	Rattus norvegicus mRNA for mitochondrial adenine nucleotide translocator
19063 K				1327	D12770	
19069 A,L		339	AA943737		ESTs	
19073 F		34	AA800576		ESTs	
19075 B,J		1275	AJ236473		ESTs	Moderately similar to cysteine-rich hydrophobic 1 [M.musculus]
19085 A,J		2441	AA892598		ESTs	
19086 A,J		2441	AA892598		ESTs	
19103 A		36	AA800797		ESTs	Highly similar to HG14_MOUSE NONHISTONE CHROMOSOMAL PROTEIN HMG-14 [M.musculus]
19105 E		162	AA859230			

TABLE 1

GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number
19121_P	608	A1044101			ESTs	1650775
19150_C	8	AA7939461			ESTs	
19158_B	140	AA851953		Moderately similar to hypothetical protein [H.sapiens]	ESTs	
19184_J		1022_A1178025		ESTs, Highly similar to TGIF_MOUSE_5'-TG-3' INTERACTING FACTOR [M.musculus]	ESTs	
19211_N		136_AA851329			ESTs	
19230_R		646_A1059604			ESTs	
19241_I		1666_NM_019206	Serine/threonine kinase 10	Serine/threonine kinase 10	ESTs	
19252_N		NM_019382	anti-oxidant protein 2	anti-oxidant protein 2	ESTs	
19255_K		1406_M15562		Rat (diabetic BB) MHC class II alpha chain RT1.D alpha (u)	ESTs	
19256_K		1406_M15562		Rat (diabetic BB) MHC class II alpha chain RT1.D alpha (u)	ESTs	
19258_O		287_AA900613		Rat (diabetic BB) MHC class II alpha chain RT1.D alpha (u)	ESTs	
19261_O		741_A1102943			ESTs	
19264_C,DR		743_A1103078			ESTs	
19292_K		445_AA997323			ESTs	
19298_A,DI		1272_A1236338		ESTs, Weakly similar to NHPX_RAT NHP2/RS6 FAMILY PROTEIN	ESTs	
19315_E		1144_A1231010		YEL028W HOMOLOG [R.norvegicus]	EST	
19363_A,F		954_A1176247		Moderately similar to unnamed protein product [H.sapiens]	ESTs	
19373_N		1684_NM_021266	Hyaluronan mediated motility receptor (RHAMM)	Hyaluronan mediated motility receptor (RHAMM)	ESTs	

TABLE 1

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GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title
19377 I	180 AA859971				ESTs, Moderately similar to Rl3_RAT 60S RIBOSOMAL PROTEIN L3 [R.norvegicus]
19388 F	206 AA891032				EST
19392 M	1592 NM_012998		Arginine and proline metabolism, Biosynthesis and degradation of glycoprotein	Protein disulfide isomerase (Prolyl 4-hydroxylase, beta polypeptide)	Protein disulfide isomerase (Prolyl 4-hydroxylase, beta polypeptide)
19410 B,Q	268 AA893687				ESTs, Moderately similar to AC006978_1 supported by human and rodent ESTs [H.sapiens]
19411 M,P	268 AA893667				ESTs, Moderately similar to AC006978_1 supported by human and rodent ESTs [H.sapiens]
19412 B,Q	120 AA849222				ESTs, Moderately similar to AC006978_1 supported by human and rodent ESTs [H.sapiens]
19444 P	309 AA924993				ESTs
19458 E	462 AA998345				EST
19465 K	630 AI045881				EST
19469 A,P	231 AA892112				ESTs, Weakly similar to proline dehydrogenase [M.musculus]
19470 A	1203 AI233266				ESTs, Weakly similar to proline dehydrogenase [M.musculus]
19476 O	1188 AI232612				ESTs
19503 P	116 AA848639				ESTs, Moderately similar to vascular endothelial growth factor D [M.musculus]
19508 A	1114 AI228698				EST

TABLE 1

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc-ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number
19512 M		855	AI160612		Rattus norvegicus adipocyte lipid-binding protein (ALBP) mRNA, complete cds		1650775
19513 R		1100	AI229035		ESTs		
					ESTs, Highly similar to ATP binding protein [H sapiens]		
19566 E		112	AA819879		ESTs		
19591 S		559	AI012747		EST		
19605 E,L		97	AA819172		EST		
19641 J		663	AI071181		EST		
					ESTs, Rattus norvegicus reinoid X receptor gamma (RXRgamma) mRNA, partial cds		
19650 H		486	AF016387		Rattus norvegicus mRNA for SH2-containing inositol phosphatase 2 (SHIP2), complete cds		
19669 R		1740	NM_022944		protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	
19671 B,Q		1656	NM_017309		Rat mRNA for type I thyroxine deiodinase	Rat mRNA for type I thyroxine deiodinase	
19678 A		1733	NM_021653		Thyroxine deiodinase, type I	Thyroxine deiodinase, type I	
19679 A		1733	NM_021653		membrane cofactor protein	membrane cofactor protein	
19715 M		1662	NM_019190		ESTs	ESTs	
19728 O		872	AI170394		ESTs	ESTs	
19729 A		87	AA818910		ESTs	ESTs	
19732 G		1262	AI236066		ESTs	ESTs	
19762 R		272	AA889113		ESTs	ESTs	
19768 I		231	AA8892373		ESTs	ESTs	
19787 H		1304	AI638994		ESTs	ESTs	

TABLE 1 Document Number 1650775

GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigenes Cluster Title
19824 O		1688 NM_021750	Taurine and hypotaurine metabolism	HHs:cysteine sulfinate acid decarboxylase-related protein 2	Rattus norvegicus brain mRNA for cysteine-sulfinate decarboxylase	
19825 O		1688 NM_021750	Taurine and hypotaurine metabolism	HHs:cysteine sulfinate acid decarboxylase-related protein 2	Rattus norvegicus brain mRNA for cysteine-sulfinate decarboxylase	
19830 A		853 A169529			ESTs, Weakly similar to 3OSB_RAT 3-OXO-5-BETA-STEROID 4-DEHYDROGENASE [R.norvegicus]	
19843 A		1308 A1639055			EST	
19909 A		1315 A1639310			EST	
19940 C		1254 A1235689			ESTs, Moderately similar to pescadillo [H.sapiens]	
19952 A		1310 A1639108			ESTs, Moderately similar to dj967N21.3 [H.sapiens]	
20016 B		1312 A1639158			Rattus norvegicus Nopp140 associated protein (NAP65) mRNA, complete cds	
20035 A		1689 NM_021754			EST	
20038 S		278 AA899797			ESTs	
20041 K		787 A1112161			ESTs, Highly similar to R32184_3 [H.sapiens]	
20063 E.L.		313 AA925063			EST, Highly similar to A42772 mdm2 protein - rat [R.norvegicus]	
20082 C		1316 A1639488			ESTs	
20088 A		246 AA892866			Rattus norvegicus pleiotropic regulator 1 (PLRG1) mRNA, complete cds	
20090 R		1690 NM_021757			EST, Moderately similar to TNF ζ MOUSE LYMPHOTOXIN- β 1A [M.musculus]	
20119 P		1033 A1178533				

TABLE 1

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
20134_P		1692_NM_021852			Rattus norvegicus EH domain binding protein epsin 2 mRNA, complete cds	
20161_A,B		1691_NM_021836			R.norvegicus pJnB gene	
20200_M		1693_NM_022194			Rat interleukin 1 receptor antagonist gene, complete cds	
20282_H		1648_NM_017274	Glycerolipid metabolism	glycerol-3-phosphate acyltransferase, mitochondrial	Rattus norvegicus gene for L-gulono-gamma-lactone oxidase	
20299_A,D		1694_NM_022220			EST	
20350_L,Q		1186_Ai232552			K-kininogen, differential splicing leads to HMW Kring	
20354_B,N,Q		1404_M14369			Rattus norvegicus mRNA for ATP-stimulated glucocorticoid-receptor translocation promoter, complete cds	
20380_E,G		1330_D16102	Glycerolipid metabolism	glycerol kinase	ESTs, Moderately similar to SYM_HUMAN METHIONYL-TRNA SYNTHETASE [H.sapiens]	
20397_A,E		1151_Ai231226			Rattus norvegicus JE/MCP-1 mRNA, complete cds	
20449_A,C,I		1494_X17053		Small inducible gene JE	ESTs	
20456_A,C		1355_H31144			Rattus norvegicus mRNA for organic anion transporting polypeptide 4 (slc21a10 gene)	
20502_A,F		370_AA945533			Rattus norvegicus mRNA for organic anion transporting polypeptide 4 (slc21a10 gene)	
20503_A,C,E		864_Ai169779				

TABLE 1

GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	
					GLYC01/ Gluconeogenesis, Purine metabolism, Pyruvate metabolism	Pyruvate kinase, liver and RBC ESTs, Moderately similar to podocalyxin [R.norvegicus]
20513 A	1554 NM_012624			Pyruvate kinase, liver and RBC		
20522 P	224 AA891842					
20523 C,P	224 AA891842					
20529 F,M,P	1644 NM_017208		lipopolysaccharide binding protein	Rattus norvegicus carnitine octanoyltransferase mRNA, complete cds		
20555 G	1458 U26033			sodium channel, voltage-gated, type I, beta polypeptide	sodium channel, voltage-gated, type I, beta polypeptide	
20579 O	1654 NM_017288			Protein 9 K homologous to calcium- binding protein	Protein 9 Ka homologous to calcium- binding protein	
20589 I	1553 NM_012618		Alanine and aspartate metabolism, Arginine and proline metabolism, Urea cycle and metabolism of amino groups	Arginosuccinate synthetase 1	Arginosuccinate synthetase 1	
20597 S	1489 X12459					
20644 I	996 AI176990					ESTs, Highly similar to SRPR_HUMAN SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT [H.sapiens]
20651 P	1460 U368992					Cytochrome P450
20684 C	1361 H32977					ESTs
20694 A	442 AAA997048					ESTs

TABLE 1

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
20989 N		1519 X89561			Rat alpha-fibrinogen mRNA, 3' end	
20701 A,B,F,Q		197 AA875097		Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily I (aromatic compound-inducible), member A2 (Q42, form d)	Rat alpha-fibrinogen mRNA, 3' end
20705 A,D		1541 NM_012541			Rattus norvegicus brain digoxin carrier protein mRNA, complete cds	Cytochrome P450, subfamily I (aromatic compound-inducible), member A2 (Q42, form d)
20707 A,D,K		1481 U88036			Rattus norvegicus mRNA for NORBIN, complete cds	Rattus norvegicus brain digoxin carrier protein mRNA, complete cds
20708 C,F		476 AB006461		Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
20711 E,K		1622 NM_016999		Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
20713 K		1622 NM_016999		Tryptophan metabolism	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
20714 K		1622 NM_016999		Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
20715 E,N		1622 NM_016999		Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
20734 A		1672 NM_019283			antigen identified by monoclonal antibodies 4F2	antigen identified by monoclonal antibodies 4F2
20735 A,C,D		1672 NM_019283			antigen identified by monoclonal antibodies 4F2	antigen identified by monoclonal antibodies 4F2
20741 F		502 AF084186				R.norvegicus mRNA for alpha II spectrin

TABLE 1

GI/GC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster/Title
20744 K				Alanine and aspartate metabolism, Arginine and proline metabolism, Cysteine metabolism, Glutamate metabolism, Phenylalanine, tyrosine and tryptophan biosynthesis, Tyrosine metabolism	Glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase, cytosolic) see also DMgh12	Glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase, cytosolic) see also DMgh12
20755 I		1545 NM_012571	1587 NM_012923	Cyclin G1	Cyclin G1	Cyclin G1
20757 A			1587 NM_012923	Cyclin G1	Cyclin G1	Rattus norvegicus protein arginine N-methyltransferase (PRMT1) mRNA, complete cds
20772 A,F			1468 U60882			ESTs, Moderately similar to HS9B, RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus]
20795 J		355 AA944397	egf, ego, i2, i3, i6, insulin, inter act6-1, nfgf, pdgf, ipo	Murine leukemia viral (v-raf-1) oncogene homolog 1 (3611-MSV)	Murine leukemia viral (v-raf-1) oncogene homolog 1 (3611-MSV)	Rattus norvegicus mRNA for APEX nuclelease, complete cds
20799 H		1405 M15428		Apurinic/apyrimidinic endonuclease 1		Rattus norvegicus Sprague-Dawley transketolase mRNA, complete cds
20801 A,I		1723 NM_024148		HMr:transketolase		Rattus norvegicus Sprague-Dawley transketolase mRNA, complete cds
20803 K		1707 NM_022592	Pentose phosphate cycle	HMr:transketolase		ESTs, Highly similar to RL1X, RAT 60S RIBOSOMAL PROTEIN L18A [R.norvegicus]
20804 K		1707 NM_022592	Pentose phosphate cycle	HMr:transketolase		
20810 A		1493 X14181				

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GLOC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
20817 G		558	AJ012589	Glutathione metabolism	glutathione S-transferase, pi 2	
20818 G		1485	X02904	Glutathione metabolism	glutathione S-transferase, pi 2	
20843 C,D		13	AA790545		ESTs, Weakly similar to TCPA_RATT-COMPLEX PROTEIN 1, ALPHA SUBUNIT [R.norvegicus]	
20846 E,N		1147	A1231140		ESTs, Highly similar to RL2B_HUMAN 60S RIBOSOMAL PROTEIN L23A [R.norvegicus]	
20849 F,I		1487	X05566		ESTs, mRNA for myosin regulatory light chain (RLC)	
20851 E		1614	NM_013214	Fatty acid metabolism,	acyl-CoA hydrolase	
20855 S		1613	NM_013200	Glycerolipid metabolism	Carnitine palmitoyltransferase 1 beta, muscle isoform	
20856 S		1613	NM_013200	Fatty acid metabolism,	Carnitine palmitoyltransferase 1 beta, muscle isoform	
20864 G,K,P		1615	NM_013215	Glycerolipid metabolism	Carnitine palmitoyltransferase 1 beta, muscle isoform	
20873 G		1000	A1177042		afatoxin B1 aldehyde reductase	
20874 A		1116	A1229789		ESTs, Highly similar to RS19_RAT 40S RIBOSOMAL PROTEIN S19 [R.norvegicus]	
20879 I		1511	X65296		ESTs, Moderately similar to KIAA0952 protein [H.sapiens]	
20889 A		1563	NM_012716		R.norvegicus mRNA for pi 6.1 esterase (ES-10)	
20891 A,C,I		852	A1169337		Solute carrier 16 (monocarboxylic acid transporter), member 1	
20897 I		945	A1175812		ESTs, Highly similar to CopA protein [M.musculus]	

TABLE 1
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GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
20914_B		1412 M23995		Aldehyde dehydrogenase 1 (phenobarbital inducible)	Aldehyde dehydrogenase 1 (phenobarbital inducible)
20915_KQ		1730 NM_017272		Aldehyde dehydrogenase 1 (phenobarbital inducible)	Aldehyde dehydrogenase 1 (phenobarbital inducible)
20830_E		473 AB004096	Fatty acid metabolism, Tryptophan metabolism	Cytochrom P450 Lanosterol 14 alpha- demethylase	Cytochrom P450 Lanosterol 14 alpha- demethylase
20850_I		7 AA799323			ESTs, Moderately similar to PLEK_HUMAN PLECKSTRIN [H.sapiens]
20871_H		15 AA798576			ESTs, Weakly similar to nucleolar RNA helicase II/Gu [M.musculus]
20875_H		16 AA799599			ESTs
20980_E		18 AA799633			ESTs
20983_F		619 A044900		Acyl CoA synthetase, long chain	Acyl CoA synthetase, long chain
20986_G		280 AA883242		Acyl CoA synthetase, long chain	Acyl CoA synthetase, long chain
20993_R		1041 AI178741			ESTs, Weakly similar to serine protease [R.norvegicus]
20998_S		24 AA799803			ESTs, Weakly similar to serine protease [R.norvegicus]
21010_S		318 AA925306	Alanine and aspartate metabolism	HMr:carnitine acetyltransferase	ESTs
21014_P		1376 J03914	Glutathione metabolism	Glutathione S-transferase, mu type 2 (Yb2)	Glutathione-S-transferase, mu type 2 (Yb2)
21025_A		163 AA859241		synaptotagmin 2 binding protein	Rattus norvegicus NPW16 mRNA, complete cds
21039_B		1373 J03190	Glycine, serine and threonine metabolism	HHs:aminolevulinate, delta-, synthase 1	Rat 5-aminolevulinate synthase mRNA, complete cds
21040_E		546 AI011734	Glycine, serine and threonine metabolism	HHs:aminolevulinate, delta-, synthase 1	Rat 5-aminolevulinate synthase mRNA, complete cds

TABLE 1

Glac ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number 1650775
21060		547	AJ011746			ESTs, Weakly similar to BACRTC10.a [D.melanogaster]	
21068 E		943	AJ175675			ESTs, Highly similar to RB24_MOUSE RAS-RELATED PROTEIN RAB-24 [M.musculus]	
21075 P		1706	NM_022584	thioredoxin reductase 2	Rattus norvegicus thioredoxin reductase (TrxR2) mRNA, nuclear gene encoding mitochondrial protein, complete cds		
21078 K		1617	NM_016886	Fatty acid metabolism, Propanoate metabolism, Valine, leucine and isoleucine degradation, beta- Alanine metabolism	Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight-chain		
21088 A,F		966	AJ176472			ESTs	
21091 E		1289	AJ236972			ESTs, Weakly similar to predicted using GeneFinder [C.elegans]	
21097 A,H,N		1400	M12112		Angiotensinogen	Rat angiotensinogen (PAT) gene	
21098 N		344	AA943892		Angiotensinogen	Rat angiotensinogen (PAT) gene	
21125 A		114	AA848437			ESTs	
21130 J		959	AJ176298			ESTs	
21150 A		119	AA848826			ESTs	
21157 A		383	AA946189			ESTs	
21164 O,S		810	AJ137488			ESTs	
21175 H		768	AJ105113			ESTs	
21184 K		709	AJ101206			ESTs	
21209 A,E		913	AJ171772			ESTs	
21228 K,M		615	AJ044404			ESTs	

TABLE 1

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number
21238 K		1719 NM_024125		IL6, interact-6-1	Liver activating protein (LAP, also NF-IL6, nuclear factor-IL6, previously designated TCF5)	Rai sfb mRNA for silencer factor B	1650775
21256 Q		1029 AA178491				ESTs	
21275 L		125 AAB49796				ESTs	
21281 B,E,M		1231 AA234090			ESTs, Moderately similar to hypothetical protein [H.sapiens]		
21285 P		126 AA849898			EST		
21305 G		258 AA883082			ESTs		
21321 H		1227 AA233902			ESTs		
21341 A,S		129 AA850195			ESTs		
21354 S		277 AA889721			ESTs		
21380 J		35 AA800739			ESTs, Weakly similar to /prediction		
21382 N		375 AA945708		Arginine and proline metabolism, Glycine, serine and threonine metabolism, Histidine metabolism, Phenylalanine metabolism, Tryptophan metabolism, Tyrosine metabolism	ESTs		
21396 A		1612 NM_013198			Monoamine oxidase B	Monoamine oxidase B	
21414 P		1255 AA235842			ESTs		
21416 I		37 AA800982			ESTs, Highly similar to TALI_MOUSE		
21421 N		1664 NM_019196		multiple PDZ domain protein	TALIN [M.musculus]		
21443 P,Q		1671 NM_019282		complement component 1, q subcomponent, beta polypeptide	multiple PDZ domain protein complement component 1, q subcomponent, beta polypeptide		

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GLGC ID	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title
21444_Q	1671 NM_019262			complement component 1, q subcomponent, beta polypeptide	complement component 1, q subcomponent, beta polypeptide
21445_M_P	1388 L18948	311 AA2925049			Rattus norvegicus intracellular calcium-binding protein (MRP14) mRNA, complete cds
21458_C		951 A1176061			ESTs
21467_N		137 AA851343			ESTs, Weakly similar to taxolene-induced gene 2 [H.sapiens]
21471_A		1097 A1228729			ESTs
21535_R		707 A1101159			ESTs
21567_R		762 A1104683			ESTs
21570_B		146 AA852038			ESTs
21574_N		1499 X56298	Biosynthesis and degradation of glycoprotein	HHs:ribophorin II	ribophorin II mRNA
21575_E		1521 X97772			R.norvegicus mRNA for D-3-phosphoglycerale dehydrogenase
21586_G_I		1507 X61381			Rattus norvegicus interferon-inducible protein variant 10 mRNA, complete cds
21657_B		863 A1168751			Rattus norvegicus interferon-inducible protein variant 10 mRNA, complete cds
21660_M		968 A1176479			Rattus norvegicus interferon-inducible protein variant 10 mRNA, complete cds
21661_M		1635 NM_017126		ferredoxin 1	ferredoxin 1
21663_B		222 AA8891789			ESTs
21672_C					CCAAT/enhancerbinding, protein (C/EBP) delta
21682_P_Q		1609 NM_013154			CCAAT/enhancerbinding, protein (C/EBP) delta
21683_P		1609 NM_013154			CCAAT/enhancerbinding, protein (C/EBP) delta

TABLE 1

GLGC ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number 1680775
21695_A_I	240 AA892506			ESTs, Weakly similar to coronin-like protein [R.norvegicus]		
21696_C	1724 NM_024152			Rattus norvegicus ADP-ribosylation factor 6 mRNA, complete cds		
21707_A,C,E,N	176 AA859722			ESTs		
21709_Q	1334 D28683		HSPENDOTHELIN-CONVERTING ENZYME 1	Rat mRNA for endothelin-converting enzyme, complete cds		
21717_E	131 AA850480			ESTs		
21740_B,M,Q	986 Al176810			ESTs		
21798_K	329 AA926365			ESTs, Moderately similar to AF45827_1 CGI-69 protein [H.sapiens]		
21799_E	730 Al102576			ESTs		
21828_I				Rattus norvegicus homocysteine respondent protein HCYP2 mRNA, complete cds		
21823_E	491 AF0365317 1119 Al229906			ESTs		
21883_E		1302 Al0237713		ESTs, Moderately similar to Y101_HUMAN HYPOTHEICAL PROTEIN KIAA0101 [H.sapiens]		
21909_H		210 AA891161		ESTs		
21950_G		570 Al013861		Rattus norvegicus 3-hydroxyisobutyrate mRNA, 3' end		
21976_R		379 AA946011		ESTs		
21977_A,G		1432 S46785		Rattus norvegicus insulin-like growth factor binding protein complex acid-labile subunit gene, complete cds		

TABLE 1
Document Number 165076

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title
21978 A,M		298 AA924289			Rattus norvegicus insulin-like growth factor binding protein complex acid-labile subunit gene, complete cds	
21980 H		264 AA883454			ESTs	
22038 A,C,D		1297 A 237609			ESTs	
22042 P		390 AA946476			ESTs	
22046 S		331 AA942726			ESTs, Weakly similar to predicted using Genefinder [C. elegans]	
22051 E		275 AA889498			ESTs, Highly similar to serine protease [H.sapiens]	
22077 A		1003 A 177099			ESTs, Moderately similar to Bl54_MOUSE BRAIN PROTEIN 154 [M.musculus]	
22099 A		727 A 102258			ESTs	
22244 J		223 AA891790			ESTs, Weakly similar to predicted using Genefinder [C. elegans]	
22335 R		887 A 170821			ESTs	
22451 B,E,Q		521 A 009115			ESTs	
22477 J		753 A 03730			ESTs	
22497 A,C		1031 A 178527			ESTs	
22204 K		886 A 170820			ESTs	
22212 A		1268 A 236294			ESTs, Highly similar to translation initiation factor eIF6 [M.musculus]	
22224 S		323 AA925869			ESTs, Moderately similar to AF15422_1 GDP-mannose pyrophosphorylase A [H.sapiens]	
22235 L		294 AA924152			ESTs	
22266 E,K		373 AA945601				

TABLE 1
Document Number: 1650775

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title
22321 B,I,M,Q		1372	J02962		Rat IgE binding protein mRNA, complete cds	
22338 A		345	AA943896		ESTs	
22368 A,Q		348	AA944157		ESTs	
22370 S		349	AA944158		ESTs	
22375 R		1121	AI230046	Glycolysis / Gluconeogenesis, Pentose phosphate cycle, Starch and sucrose metabolism	ESTs, Highly similar to G6PI_MOUSE GLUCOSE-6-PHOSPHATE ISOMERASE [M.musculus]	
22379 L		1156	AI231448	Glucose phosphate isomerase	ESTs, Weakly similar to es_64 [M.musculus]	
22392 S		351	AA944269		ESTs	
22395 A		352	AA944289		ESTs	
22397 F		353	AA944304		ESTs	
22412 E		1702	NM_022392	Rattus norvegicus growth response protein (CL-6) mRNA, complete cds	ESTs	
22416 S		354	AA944380		ESTs	
22432 A,C		895	AI171263		ESTs, Highly similar to FBRL_MOUSE FIBRILLARIN [M.musculus]	
22443 J		1284	AI236761		ESTs	
22457 A		358	AA944572		ESTs, Weakly similar to T2D7_RAT TRANSCRIPTION INITIATION FACTOR TFIID 31 KD SUBUNIT [R.norvegicus]	
22487 A,F,H		731	AI02578		ESTs, Highly similar to 149623 Mouse primary response gene B94 mRNA, 3end - mouse [M.musculus]	
22503 L		359	AA944823		ESTs	
22512 M,P		1531	NM_012488	Alpha-2-macroglobulin	Alpha-2-macroglobulin	
22513 F,M		1531	NM_012488	Alpha-2-macroglobulin	Alpha-2-macroglobulin	

TABLE 1

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
22514 M,P		1531 NM_012488		Alpha-2-macroglobulin	Alpha-2-macroglobulin	
22515 M		1531 NM_012488		Alpha-2-macroglobulin	Alpha-2-macroglobulin	
22516 M,P		796 NM_0113046		Alpha-2-macroglobulin	Alpha-2-macroglobulin	
22531 E		361 AA944943			ESTs	
22534 E		310 AA925045			ESTs	
22540 R		304 AA924630		Glyoxylate and dicarboxylate metabolism, Pyruvate metabolism	HHs_glyoxylate reductase/dihydroxypyruvate reductase	ESTs, Weakly similar to SERA_RAT_D-3 PHOSPHOGLYCERATE DEHYDROGENASE [R. norvegicus]
22548 L		364 AA945031				
22554 A,E,G,O		366 AA945076				ESTs
22558 A,E		368 AA945123		Hydroxyacid oxidase 1 (glycolate oxidase)	Hydroxyacid oxidase 1 (glycolate oxidase)	EST
22559 A,D		839 AI169007				ESTs
22566 E		1007 AI177122				ESTs
22569 A		1073 AI179979				ESTs
22570 R		369 AA945238				ESTs
22582 A,G		1605 NM_013120		Glucokinase regulatory protein	Glucokinase regulatory protein	
22588 M		811 AI137506				
22603 E		494 AF044574				
22619 B,E,Q		531 AU009825				ESTs
22620 S		316 AA925258				ESTs
22626 J		374 AA945704				ESTs
22679 A		332 AA942731				ESTs
22681 J		357 AA944413				ESTs
22683 A		970 AI176484				ESTs

TABLE 1
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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title
22696 H		1032	A1178531			ESTs
22713 K		378	AA945804			ESTs
22717 L		1267	A1235948		ESTs, Highly similar to elastin [R.norvegicus]	
22722 O		804	A1137211		ESTs	
22725 Q		283	AA900506		ESTs, Highly similar to TS24_MOUSE PROTEIN TSG24 [M.musculus]	
22737 S		485	AA998660		ESTs	
22770 A		387	AA946428		ESTs	
22806 E,Q		551	A1012174		ESTs, Moderately similar to hypothetical protein [H.sapiens]	
22835 L		1079	A1180367		Rattus norvegicus small zinc finger-like protein (TIM10), mRNA, complete cds	
22840 N		528	A1009676		ESTs	
22862 H		227	AA891944		ESTs	
22876 C		917	A1172041		ESTs, Moderately similar to CGI-137 protein [H.sapiens]	
22877 A,C,D		1045	A1178819		ESTs, Moderately similar to CGI-137 protein [H.sapiens]	
22897 P		290	AA891107		ESTs	
22898 L,P		290	AA891107		ESTs	
22906 L,N		944	A1175790		ESTs, Moderately similar to cell death activator CIDE-A [M.musculus]	
22918 B,Q		29	AA800243		ESTs	
22928 A,F		328	AA926262		ESTs	
22929 A,L		670	A1071578		ESTs	
22930 A		670	A1071578		ESTs	
22931 A		777	A1105417		ESTs	

TABLE 1

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number
22957 R		764	AJ104897		IHMn:milogen activated protein kinase kinase 3	ESTs, Moderately similar to meningioma expressed antigen 11 [H.sapiens]	1650775
22961 E		1064	AJ179519			ESTs	
22966 B		1128	AJ230320			ESTs	
23000 H		178	A4859933			ESTs	
23005 F,P		334	A4942770			ESTs, Weakly similar to ACTC_HUMAN ACTIN, ALPHA CARDIAC [R.norvegicus]	
23013 I			1137	AJ230743		ESTs	
23030 L			305	A4924763		ESTs	
23032 K			976	AJ176586		ESTs	
23033 G			179	A4859938		ESTs, Weakly similar to URB1_RAT DNA BINDING PROTEIN URE-B1 [R.norvegicus]	
23043 N			1051	AJ178968		Rattus norvegicus hyaluronidase (Hya2)	
23044 A,H			490	AF034218		mRNA, complete cds	
23047 H			230	AA892027		ESTs	
23075 A			844	AJ169166		ESTs	
23077 H			1015	AJ177489		ESTs	
23082 A			980	AJ176648		ESTs, Highly similar to mm-Mago	
23099 C			789	AJ112365	Minichromosome maintenance deficient 4 homolog (S.cerevisiae)	[M.musculus]	
23106 Q,R			825	AJ145081		ESTs, Highly similar to Cdc21 [H.sapiens]	
23120 C,D			1070	AJ179857		ESTs, Weakly similar to UB5D_RAT UBIQUITIN-CONJUGATING ENZYME E2-17 KD 4 [R.norvegicus]	

TABLE 1

GLC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc. ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number
23125 B.Q		1172	AJ232266			ESTs	1650775
23128 E		561	AJ013011			ESTs	
23139 H		1076	AJ180040			ESTs	
23160 C.L		960	AJ176319	HMM:nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, beta	Rattus norvegicus L-kappa-B-beta mRNA, complete cds		
23170 E		850	AJ169317		ESTs, Weakly similar to C43H8.1 [C.elegans]		
23173 I			312	AA925057	ESTs, Highly similar to CRIP MOUSE CYSTEINE-RICH INTESTINAL PROTEIN [R.norvegicus]		
23182 F.N			1141	AJ230981	ESTs		
23183 O			819	AJ144586	Rattus norvegicus eveetin-1 (EV/T1) mRNA, complete cds		
23184 C			974	AJ176554	ESTs		
23220 O		1319	AJ000347	Sulfur metabolism	HMM:bisphosphate 3'-nucleotidase 1 bisphosphate nucleotidase		
23229 C		1229	AJ234038		ESTs		
23230 A.H.N		1286	AJ236146		ESTs		
23243 E		138	AA651803		ESTs		
23245 Q			1066	AJ179570	ESTs		
23260 C.D			856	AJ169617	ESTs, Highly similar to Bop1 [M.musculus]		
23261 A,C,D			314	AA925145	ESTs		
23299 C			989	AJ176839	ESTs		
23302 I,N		1516	X78849	Arginine and proline metabolism	HMM:procollagen-proline, 2'-oxoglutarate 4-dioxygenase (prolyl 4-hydroxylase), alpha 1 polypeptide R.norvegicus mRNA for prolyl 4-hydroxylase alpha subunit		

TABLE 1

GLGC ID	Nucleotide Sequence ID	GenBank AccID	Pathways	Known Gene Name	Unigene Cluster Title
23304_E	1153 AI231310		HMM/procollagen-proline, 2'-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	R.norvegicus mRNA for prolyl 4-hydroxylase alpha subunit	ESTs
23315_E,R	239 AA892425			Rattus norvegicus alkar mRNA for androgen-inducible aldehyde reductase, complete cds	ESTs
23321_A	247 AA892821			Rattus norvegicus alkar mRNA for androgen-inducible aldehyde reductase, complete cds	ESTs
23322_A	247 AA892821			Rattus norvegicus alkar mRNA for androgen-inducible aldehyde reductase, complete cds	ESTs
23324_E	181 AA865980			TCPA_RAT_T-COMPLEX PROTEIN 1, ALPHA SUBUNIT [R.norvegicus]	ESTs
23325_A	928 AI172405			TCPA_RAT_T-COMPLEX PROTEIN 1, ALPHA SUBUNIT [R.norvegicus]	ESTs
23331_J	1210 AI233457			Ras homolog enriched in brain [M.musculus]	ESTs
23337_E,O	520 AI009096			Rat homolog enriched in brain	ESTs
23362_O	1616 NM_013216			Rat homolog enriched in brain	ESTs
23380_A	141 AA851961			Rat homolog enriched in brain	ESTs
23390_D,G	927 AI172328			TCPA_RAT_T-COMPLEX PROTEIN 1, ALPHA SUBUNIT [R.norvegicus]	ESTs
23435_C	1112 AU295602			Highly similar to KIAA0601 protein [H.sapiens]	ESTs
23437_A,O	661 AU071166			Highly similar to F25965.1	ESTs
23438_C,J	745 AI103101			Highly similar to F25965.1 [H.sapiens]	ESTs

TABLE 1

Document Number 1650775						
GLGC ID	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title	
23445_A,D,F	1571 NM_012792	Flavin-containing monooxygenase 1		Flavin-containing monooxygenase 1	Flavin-containing monooxygenase 1	
23448_B	315 AA925167	ESTs		ESTs	ESTs	
23449_B,Q	987 A1176828	ESTs		acidic calponin	acidic calponin	
23491_H,N,O	1681 NM_018359	ESTs		ESTs	ESTs	
23494_N	888 A1170967	EST		ESTs	ESTs	
23499_A	393 AA955249	ESTs		ESTs	ESTs	
23500_A,S	183 AA860010	ESTs		ESTs	ESTs	
23511_A	1697 NM_022294	ESTs		ESTs	ESTs	
23515_L	1063 A1179498	ESTs		ESTs	ESTs	
23522_A,F	1552 NM_012615	Arginine and proline metabolism,Urea cycle and metabolism of amino groups		Ornithine decarboxylase	Ornithine decarboxylase	
23523_A	1552 NM_012615	Arginine and proline metabolism,Urea cycle and metabolism of amino groups		Ornithine decarboxylase	Ornithine decarboxylase	
23555_M,P	394 AA955443	ESTs		ESTs	ESTs	
23558_A	400 AA956170	ESTs, Weakly similar to NDKA, RAT NUCLEOSIDE DIPHOSPHATE KINASE A [Rnorvegicus]		ESTs	ESTs	
23567_J	1042 A1178746	ESTs		ESTs	ESTs	
23584_A,B	392 AA955071	ESTs		ESTs	ESTs	
23587_J	977 A1176598	ESTs		ESTs	ESTs	

TABLE I

TABLE I						
Gene ID	Compassion Code	Nucleotide Sequence ID	GenBank Acc. ID	Pathways	Known Gene Name	Unigene Cluster Title
23606_H.N		1714 NM_022867				Watsonia microtubule-associated proteins 1A and 1B light chain 3 subunit mRNA, complete cds
23608_E	23612_A	1201 AI233190 880 AI10751				Rattus norvegicus microtubule-associated proteins 1A and 1B light chain 3 subunit mRNA, complete cds
23626_N		395 Aa955540				Rattus norvegicus microtubule-associated proteins 1A and 1B light chain 3 subunit mRNA, complete cds
23627_S		628 AI045624				ESTs
23633_A		706 AI10130				ESTs
23651_I		1582 NM_012881				Sialoprotein (osteopontin)
23656_R		616 AI044533				ESTs
23678_C		1674 NM_019290				B-cell translocation gene 3
23679_A.C.D.F		1674 NM_019290				B-cell translocation gene 3
23698_E		1532 NM_012489				B-cell translocation gene 3
23709_H.K		1603 NM_013113				Acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolease A, peroxisomal
23710_H		1135 AI230614				ATPase Na+/K+ transporting beta 1 polypeptide
23711_H		1603 NM_013113				ATPase Na+/K+ transporting beta 1 polypeptide
23762_R		404 AA956431				ESTs, Highly similar to Lsm5 protein [H sapiens]
23767_A		1295 AI237207				ESTs
23843_E.R		412 AA957410				ESTs
23847_B		405 AA956723				EST

TABLE 1					Document Number 1650776
GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
23864 G,I	1514 X78327			R.norvegicus (Sprague Dawley) ribosomal protein L13 mRNA	
23865 B,C	1287 AF236773			ESTs	
23868 F	1543 NM_012551		Early growth response 1	Early growth response 1	
23869 F	1543 NM_012551		Early growth response 1	Early growth response 1	
23872 F	1543 NM_012551		Early growth response 1	Early growth response 1	
			Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Histidine metabolism, Lysine degradation, Phenylalanine metabolism, Propanoate metabolism, Pyruvate metabolism		
23884 A	1422 M73714			aldehyde dehydrogenase 4, liver microsomal (class 3)	Rat microsomal aldehyde dehydrogenase mRNA, complete cds
23885 E	866 AJ170007				ESTs
23888 I	241 AA892520				ESTs
23889 M	241 AA892520				ESTs
23890 B	406 AA958864				ESTs
23945 F	409 AA957071			ESTs, Highly similar to Bcl-2-interacting protein beclin [H.sapiens]	
23955 A	1103 AI229178				ESTs
23961 A,D	1640 NM_017181		Tyrosine metabolism	fumarylacetoacetate hydrolase	ESTs
23987 O	1496 XS1615				ESTs
23989 B,Q	1072 AI179853				ESTs
24012 M,O	411 AA957335				ESTs

TABLE 1 Document Number: 1690775

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Accession ID	Pathways	Known Gene Name	Unigene Cluster Title
24024 Q		496	AF052695		Rattus norvegicus p55GDC mRNA, complete cds	
24049 G		1010	AI177341		ESTs, Highly similar to CGI-10 protein [H.sapiens]	
24051 L		414	AA957452		EST	
24079 H		935	AI175423		ESTs	
24112 O		514	AI008773		ESTs	
24126 R		415	AA957708		ESTs, Weakly similar to hypothetical protein [H.sapiens]	
24146 E		859	AI169668		ESTs	
24161 E		150	AA058888		ESTs	
24162 A		847	AI1698279		ESTs	
24200 N		555	AI0172356		ESTs	
					Rattus norvegicus tyrosine phosphatase protein tyrosine phosphatase 4a1 (PRL-1) mRNA, complete cds	
24219 A		1395	L27843		ESTs	
24227 L		871	AI170385		ESTs, Weakly similar to A1AT_RAT	
24228 M		30	AA800318		ALPHA-1-ANTIPROTEINASE PRECURSOR [R.norvegicus]	
24234 J		1469	U63923		Rattus norvegicus NADPH-dependent thioredoxin reductase (TRR1) mRNA, complete cds	
24235 A,D,J		213	AA891286		Rattus norvegicus NADPH-dependent thioredoxin reductase (TRR1) mRNA, complete cds	
24236 C,L		967	AI176473		ESTs	
24237 F,M		44	AA817726		ESTs	

TABLE 1

GLC ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number: 1650775
24246 G	419 AA963703	1593 NM_012999		ESTs, Highly similar to cell cycle protein p38-G4 homolog [H.sapiens]		
24264 A		924 A1172281		Subtilisin - like endopeptidase	ESTs	
24268 E				Rattus norvegicus nucleolar phosphoprotein of 140kD, Nopp140 mRNA, complete cds	ESTs	
24284 A	1715 NM_022869			ESTs, Highly similar to galactokinase [M.musculus]	ESTs	
24289 B,Q	399 AA955986	Galactose metabolism	Galactokinase	ESTs, Highly similar to steroidogenic acute regulatory protein [R.norvegicus]	ESTs	
24296 E	1360 H32867			ESTs		
24321 A,D,G	1178 A1232340			ESTs, Moderately similar to GTM1_RAT GLUTATHIONE S-TRANSFERASE YB1 [R.norvegicus]	ESTs	
24323 P		763 A1104798		EST		
24367 R	401 AA956247			ESTs, Highly similar to AF114169_1 nucleotide-binding protein short form [M.musculus]	ESTs	
24368 R		1090 A1180392		ESTs, Highly similar to AF114169_1 nucleotide-binding protein short form [M.musculus]	ESTs	
24369 R			346 AA944011	ESTs, Moderately similar to nucleolar protein p40 [H.sapiens]	ESTs	
24375 A,D		766 A1104979		ESTs		
24381 S		403 AA956301		ESTs		
24388 C,D,I,R		1286 A1236772		Rat mannose-binding protein C (liver) mRNA, complete cds	ESTs	
24434 A		1710 NM_022704		Rat matrin F/G mRNA, complete cds	ESTs	
24442 O		1708 NM_022967		Rat matrin F/G mRNA, complete cds	ESTs	

TABLE 1

GLGC ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name		Unigene Cluster Title
				Comparison Code	Document Number 1650775	
24453 F		1560 NM_012690		P-glycoprotein 3/ multidrug resistance 1 2, P-glycoprotein/multidrug resistance 1	P-glycoprotein 3/ multidrug resistance 1 Rat metabotropic glutamate receptor (GLUR4) mRNA, complete cds	
24458 A		1711 NM_022706				Rattus norvegicus translation elongation factor 1-delta subunit mRNA, partial cds
24501 D		1167 AI232006				Rat neurotrophin-3 (NTNF/NT-3) mRNA, complete cds
24508 E		1416 M34643				ESTs, Highly similar to RL2_RAT_60S ACIDIC RIBOSOMAL PROTEIN P2 [R.norvegicus]
24577 A		1498 X55153				
24589 E,P		1558 NM_012674		Serine protease inhibitor, kanzai type 1/ Trypsin inhibitor-like protein, pancreatic Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	Serine protease inhibitor, kanzai type 1/ Trypsin inhibitor-like protein, pancreatic Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	
24597 C		1625 NM_017040		Starch and sucrose metabolism	HM/amylase 2, pancreatic	Rat pancreatic amylase mRNA, partial coding sequence
24645 A		1484 V01225				Sprague-Dawley (clone LRB10) RAB13 mRNA, 3'end
24651 P		1426 M83678				Sprague-Dawley (clone LRB2) RAB16 mRNA, complete cds
24654 E		100 AA819333				
24670 G		1642 NM_017189		Fatty acid metabolism, Tryptophan metabolism	asialoglycoprotein receptor 2	asialoglycoprotein receptor 2
24707 E,O		1561 NM_012693		Cytochrome P450 11A2	Cytochrome P450 11A2	Cytochrome P450 11A2
24710 C		1430 M98820	interact6-1	Interleukin 1 beta	Interleukin 1 beta	Rat interleukin 1-beta mRNA, complete cds

TABLE I
Document Number 165075

GLGC ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
24721 Q	99 AA819306				ESTs
24722 G	1564 NM_012725			Plasma kallikrein	Plasma kallikrein
24771 A,G	1626 NM_017047		Cysteine metabolism, Glycine, serine and threonine metabolism, Oxidative phosphorylation	Solute carrier family 10 (sodium/bile acid cotransporter family), member 1	Solute carrier family 10 (sodium/bile acid cotransporter family), member 1
24779 F	1375 J03863			HT1s serine dehydratase	Rat serine dehydratase (SDH2) mRNA, complete cds
24810 F,G	1391 L22339		Sulfur metabolism	sulfotransferase, phenol preferring 2	Rat N-hydroxy-2-acetylaminofluorene (ST1C1) mRNA, complete cds
24811 G	1391 L22339		Sulfur metabolism	sulfotransferase, phenol preferring 2	Rat N-hydroxy-2-acetylaminofluorene (ST1C1) mRNA, complete cds
24826 P	1421 M63991		Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism		Rat thyroxine-binding globulin (TBG) mRNA, 3' end
24860 K,S	1403 M13506				
24883 A	1677 NM_019293				
25024 F	1353 E03229				
25052 A,F,M,P	1390 L22190				
25054 A	1396 L36460				
25055 K	1398 M11251				
25056 K,L	1402 M13234				
25069 F,G	1440 S82820				
25077 Q	1453 U20643				

TABLE I

Document Number 1660775						
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title
				Arginine and proline metabolism,Glycine, serine and threonine metabolism,Histidine metabolism,Phenylalanine metabolism,Tryptophan metabolism,Tyrosine metabolism,beta-Alanine metabolism		
250983 P			1473 U72632		Hsp MEMBRANE COPPER AMINE OXIDASE	
250984 J			1 AA108277		insulin receptor substrate 2	
26183 K			495 AF050159			
26198 L			1689 NM_021754			
28203 E			501 AF079873			
28246 M			1321 AJ011607			
28257 C,I			1328 D13623			
28290 M,O			1339 D42148			
28313 I			1347 DB7991			
28370 B,Q			1387 L16995			
28379 Q			1394 L26292			
28397 E			1401 M12822			
28409 E			1408 M18527			
28410 E			1409 M18528			
28411 E			1410 M18529			
28413 E			1411 M18531			
28480 A,G			1432 S46795			
28525 P			1437 S72505	Glutathione metabolism	Hsp GLUTATHIONE S-TRANSFERASE YC-1	
28567 A,J			1441 SB5184			
28615 E			1466 U58466			

TABLE 1

GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	Unigene Cluster Title	Document Number
25618 M		1470	U64705				1650775
25619 M		1470	U64705				
25632 G		1476	U75405				
25644 E		1479	U77931				
25675 A		1493	X14181				
25702 A		1502	X58465				
25705 H		1504	X58375				
25706 L		1506	X58608				
25718 IO		1508	X62145				
25725 K		1510	X62660				
25747 A,F		1518	X81448				
25768 Q		1520	X94769				
25777 E		1523	Y08355				
25802 E,I		1352	E02315				
25814 H		1686	NM_022268				
25852 L		1305	A1638988				
25892 G		1309	A1639101				
25907 J		1313	A1639167				
25938 B		1314	A1639281				
26089 E		291	AA901152				
26109 S		441	AA997009				
26123 D		511	A1008396				
26133 M		532	A1008950				
26147 E		563	A1013387				
26152 N		576	A1028938				
26190 E,R		688	A1072578				
26280 Q		1082	A1227562				
26288 E		1134	A1230577				
26320 M		1242	A1234927				

TABLE 1

GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc. ID	Pathways	Known Gene Name		Unigene Cluster Title
				Known Gene Name	Unigene Cluster Title	
263681E	1367	H34047				
263691C,D	1369	H34687				

Document Number 1650775

Comparison	Document Number 1650775
Comparison	Comparison Code
General Toxicity: Amitriptyline, ANIT, APAP, CCI4, Diclofenac, Indomethacin, Valproate, Untreated Rats, Various Vehicles, WY-14643, Cyproterone Acetate, and Estradiol	A
Hepatitis-inducing and NSAIDS: Diclofenac and Indomethacin	B
Necrosis and Fatty Liver: Carbon Tetrachloride and Valproate	C
Necrosis With and Without Fatty Liver: Carbon Tetrachloride, Valproate, and Acetaminophen	D
Protein Adduct Formers: Valproate and Diclofenac	E
ANIT	F
Late Acetaminophen	G
Early Acetaminophen	H
Late Carbon Tetrachloride	I
Early Carbon Tetrachloride	J
Late Cyproterone Acetate	K
Early Cyproterone Acetate	L
Late Diclofenac	M
Early Diclofenac	N
Estradiol	O
Late Indomethacin	P
Early Indomethacin	Q
Valproate	R
WY-14643	S

TABLE 3A: General Toxicity

Document Number 1650775

GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
21471	30.43	93.54	75	-42.67	24.83
13203	35.33	61.64	74	-31.14	29.79
19909	22.08	33.51	73	-15.41	29.38
4553	13.83	18.08	72	1.43	6.49
15301	124.27	140.5	77	5.51	36.16
20456	42.5	31.85	70	7.46	20.45
23679	57.12	66.55	72	8.07	7.49
14693	37.57	38.27	72	9.49	11.63
12471	26.73	25.33	73	9.55	21.73
923	60.74	80.74	71	9.6	6.57
15647	49.51	40.73	72	10.9	23.58
6322	45.84	55.48	70	12.42	10.76
16314	48.7	48.51	70	12.45	16.75
25052	90.08	154.89	70	14.05	18.5
2164	57.65	53.74	73	14.96	17.31
16006	58.93	36.27	80	15.18	19.39
25054	45.65	42.59	72	15.37	40.01
6410	4.65	23.5	70	15.8	61.49
23500	39.03	35.28	70	16.65	11.6
16312	39.06	24.35	75	17.24	10.59
19843	2.55	18.74	74	17.7	10.31
14996	58.1	47.71	71	20.43	22.52
16085	60.79	45.9	70	21.59	14.6
17982	49.3	27.48	70	23.22	18.41
6226	46.81	36.97	71	23.54	10.28
9326	6.05	16.52	70	24.18	25.4
15055	-7.1	34.32	70	24.3	26.9
351	94.58	92.7	71	26.37	19.43
1126	48.74	21.68	72	26.96	14.06
20161	87.17	88.37	76	27.44	26.92
8766	-14.3	48.76	75	27.97	35.81
23511	12.84	20.12	72	29.05	16
5461	77.51	74.15	71	29.28	16.66
12216	-22.58	61.28	71	29.83	80.65
5384	100.6	91.07	76	30.03	29.52
18389	43.98	46.66	74	31.53	26.82
21695	45.44	55.44	72	31.53	16.62
11357	17.28	18.76	73	31.76	16.7
14424	567.82	812.48	70	32.4	34.02
9331	60.44	27.33	70	33.81	15.06
23767	23.85	17.49	71	34.2	50.3
15862	62.08	31.33	71	34.72	12.31
20449	117.61	143.09	71	35.82	9.2
10248	68.54	26.33	77	36.88	16.24

TABLE 3A: General Toxicity Document Number 1650775

GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
23082	23.23	17.75	71	37.04	12.65
9425	17.36	27.44	71	37.87	17.12
16730	73.58	39.38	73	39.09	20.24
9583	161.94	162.1	73	39.37	25.85
11563	71.92	56.8	70	39.98	27.02
352	130.52	119.67	76	40.04	18.99
6604	24.19	16.7	74	41.3	15.53
7243	91.87	50.42	74	41.4	14.59
17709	71.49	47.04	70	41.77	28.89
1583	62.93	26.33	71	41.81	9.01
761	28.63	19.45	70	43.38	21.32
3849	81.84	39.76	71	43.61	16.59
24284	65.8	20.86	74	45.29	13.2
3207	25.59	109.41	70	45.31	54.06
21707	108.81	66.66	72	45.32	39.4
17589	85.64	50.71	71	46.93	27.53
22212	112.59	77.44	70	47.96	21.25
5175	72.78	115.19	71	48.48	31.56
7299	220.49	225.32	77	49.33	34.75
19878	3.58	46.62	75	49.59	34.93
21088	58.85	18.82	72	51.63	11.12
15892	152	118.78	75	52.52	42.58
14353	84.25	29.24	74	53.47	12.39
11527	119.25	79.46	70	54.98	27.79
13749	38.3	29.23	73	55.43	20.89
4281	38.95	21.16	70	57.15	17.8
353	194.24	177.12	76	57.46	26.37
14206	41.14	16.67	73	57.71	14.34
16080	207.65	183.99	77	58.82	28.68
6682	53.78	37.44	70	59.02	19.46
825	42.12	20.91	71	59.35	17.09
7918	90.4	45.57	71	60.65	23.06
21150	138.34	101.42	71	64.19	46.67
7531	57.13	26.96	70	64.99	18.47
22487	81.97	69.8	71	66.94	27.76
24264	112.04	51.05	72	67.41	29.12
22077	46.19	26.57	70	67.77	24.16
21209	174.43	157.48	73	70.46	46.49
20772	102.74	37.31	72	70.49	15.59
8600	33.46	36.07	72	71.84	38.68
9826	49.36	28.75	70	72	22.77
17688	108.65	39.15	70	72.62	19.69
6640	40.46	39.18	74	73.64	29.52
3074	75.98	91.66	70	73.84	44.71

TABLE 3A: General Toxicity			Document Number 1650775		
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
4473	54.98	25.48	70	74.37	21.06
354	227.5	203.23	77	74.89	23.89
23522	107.75	42.24	73	74.91	18.29
15299	176.87	143.39	75	75.35	20.66
13166	145.19	92.31	71	75.39	33.67
7936	59.06	21.73	70	76.33	18.71
17819	57.46	25.12	71	76.84	20.15
17908	191.58	159.91	71	77.06	30.42
7681	125.85	57.35	71	77.88	39.68
23633	66.31	40.72	70	78.12	28.98
19508	49.65	31.49	70	78.53	32.19
9541	166.47	123.33	72	79.59	34.68
16446	58.49	21.61	71	80.2	20.86
17377	119.83	80.06	72	82.65	37.63
20801	136.04	60.94	71	83	38.58
7352	164.48	94.53	70	83.91	38.34
2901	63.21	31.06	71	84.9	24.78
15156	85.12	43.67	71	85.31	23.45
22877	140.94	62.91	71	85.66	25.88
15207	112.17	89.27	73	85.8	32.15
9627	65.98	37.05	73	86.7	25.5
4017	71.08	40.29	70	86.72	27.99
4944	252.32	217.46	76	86.84	38.34
3073	78.22	126.03	72	87.19	58.64
5046	99.33	75.05	70	91.34	37.3
3713	66.05	38.37	71	91.52	27.81
11576	56.54	27.2	75	92.19	28.07
1246	57.52	28.55	70	92.34	25.09
15382	699.61	884.63	73	92.89	30.78
18109	105.09	108.04	71	93.58	44.98
18906	66.76	34.6	72	93.87	22.06
16324	65.53	39.09	72	94.25	27.97
7903	31.76	35.55	72	94.94	65.97
7063	179.3	93.83	74	95.16	22.48
9053	60.23	42.49	72	97.12	25.77
5813	67.41	28.11	70	97.48	35.73
9245	39.62	45.11	73	97.55	55.74
16081	293.48	225.5	78	97.81	34.89
19085	146.97	54.5	71	98.39	27.86
3189	48.18	30.77	70	99.15	55.31
12655	74.53	78.23	70	99.85	45.15
5219	54.76	44.93	70	100.79	47.29
7062	157.19	68.98	70	101.14	24.11
6820	132.9	40.9	71	101.15	18.57

TABLE 3A: General Toxicity Document Number 1650775

GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
21025	52.78	49.73	75	102	38.88
14746	72.12	42.89	70	102.6	35.3
11745	127.84	29.61	71	102.7	19.78
20035	330.62	323.46	73	105.65	47.24
12587	72.78	43.64	72	105.95	35.48
2372	89.09	42.56	70	107.07	30.91
2383	87.59	39.36	72	108.56	32.43
2532	28.55	57.57	72	109.2	73.94
11959	91.5	26.27	70	109.84	20.36
24375	200.33	108.66	72	110.42	32.85
15884	135.81	86.11	70	111.91	36.88
2576	81.51	44.81	71	112.47	36.08
23955	98.48	60.26	72	113.59	36.89
5008	152.54	61.16	71	113.65	24.98
20891	174.25	85.84	72	114.45	35.06
18390	78.44	44.36	70	116.93	42.8
1844	172.33	73.68	70	117.06	23.94
17591	177.66	76.44	70	119.35	26.88
22038	178.88	77.12	70	119.93	32.92
20874	102.83	26.99	76	120.76	19.57
17844	225.91	107.09	73	120.8	50.32
11691	80.29	49.49	73	124.21	42.81
19086	192.42	71.46	72	124.7	32.65
14937	93.31	50.67	75	125.88	34.64
20513	76.12	59.17	72	127.29	74
6037	90.3	39.56	73	127.31	44.99
12332	24.75	72.13	73	128.95	100.98
17335	99.84	36.82	73	129.97	30.57
134	71.14	58.38	77	133.41	39.47
7784	109.76	36.32	70	134.08	25.84
25567	222.63	133.25	70	134.17	40.36
4951	296.48	152.65	74	135.21	102.87
13351	87.72	56.78	76	135.45	45.49
22432	207.69	93.56	71	137.45	35.3
3075	134.78	146.57	74	138.67	65.46
16134	88.41	44.61	74	139.59	36.27
18660	99.04	62.72	74	141.07	60.13
17225	208.62	72.16	71	141.32	36.37
10509	91.25	50	70	142.42	48.95
6190	108.44	39.25	71	142.68	30.93
17393	216.6	101.01	70	144.48	27.96
22197	295.18	157.65	75	144.6	54.77
19952	98.31	43.39	75	145.63	36.13
1690	206.44	90.45	70	147.21	36.46

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox StdDev	LDA Score	Non Tox Mean	Non Tox StdDev
23044	188.12	53.18	74	148	23.7
22931	50.06	64.25	72	148.05	101.64
14776	103.46	45.74	74	148.29	40.54
14051	218.89	97.53	70	149.85	36.11
22569	103.93	53.65	76	150.14	42.57
11403	485.69	353.08	74	150.23	94.34
13762	105.01	72.99	71	151.26	47.6
14074	72.32	60.1	74	153.35	74.91
18960	120.13	59.4	71	156.6	44.43
20889	193.77	86.18	70	156.83	37.64
4084	127.09	64.08	71	158.37	49.57
18854	124.79	56.31	70	158.52	38.36
20735	294.63	147.51	80	164.19	33.2
14181	117.28	41.72	73	165.97	41.05
24883	122.66	51.37	75	165.99	38.66
15933	192.2	65.93	70	166.13	35.32
18792	112.37	55.57	73	167.2	48.33
10544	240.01	60.23	77	167.22	32.41
14208	98.76	46.96	77	167.76	48.04
20734	292.65	126.84	78	169.42	39.52
17334	283.45	131.16	76	170.46	50.64
22457	319.78	159.2	71	170.89	83.07
21978	127.23	34.44	75	172	37.41
20088	138.87	33.78	75	173.08	29.79
15300	301.38	143.25	73	174	53.02
16364	109.25	72.42	74	174.33	56.68
8829	280.85	107.19	74	174.35	39.95
1007	71.78	95.85	73	174.52	94.52
6443	130.76	76.39	77	174.54	46.87
17154	237.49	69.3	73	174.79	36.28
6473	107.85	42.8	72	175.56	60.84
2335	121.97	52.51	71	175.91	56.34
12450	90.03	92.4	75	181.36	63.89
16700	116.46	131.83	75	181.51	86.73
15955	105.87	86.17	73	183.02	74.51
23523	254.3	77.51	75	184.72	39.26
15900	300.11	139.69	72	184.95	58.44
10545	272.15	72.91	74	188.26	35.42
16982	503.02	283.02	72	188.67	203.36
12848	147.36	47.97	70	188.99	42.1
5749	219.23	62.17	70	189.76	42.51
15004	289.65	146.93	71	189.87	51.07
23075	307.83	118.82	72	190.09	58.23
23584	123.89	91.92	73	190.24	73.31

TABLE 3A: General Toxicity					Document Number 1650775
GLGC ID	Tox Mean	Tox StdDev	LDA Score	Non-Tox Mean	Non-Tox StdDev
14997	311.34	155.46	77	193.29	31.96
7617	133.32	123.53	70	193.38	108.54
11404	425.93	237.07	74	193.8	75.57
14095	145.71	64.97	77	194.48	44.06
16766	128.68	62.34	72	197.3	64.57
13757	132.12	63.33	72	197.76	47.88
3981	165.72	126.27	71	199.27	79.29
6632	374.92	164.24	76	199.58	56.28
22770	344.97	196.08	74	199.66	52.17
1099	159.6	51.35	71	200.56	47.88
15170	132.07	62.08	79	201.16	44.18
21125	104.89	85.5	74	205.52	74.23
23499	149	73.65	71	206.76	68.16
16765	131.63	64.51	74	208.95	60.5
23321	173.83	57.63	71	209.49	31.61
18908	94.04	112.32	72	209.75	126.49
4360	159.27	76.32	72	212.18	102.53
5027	165.48	78.52	73	212.59	52.82
14007	147.14	73.93	77	213.84	62.97
4719	153.89	88.13	74	216.28	70.99
9754	78.35	97.33	75	218.88	111.68
5867	342.61	167.79	70	219.32	57.15
16859	374.28	189.12	73	220.43	60.14
24434	132.32	69.32	71	226.73	56.25
22683	206.07	65.39	71	228.15	41.78
13963	218.82	179.67	72	228.18	75.69
11179	165.79	72.22	70	230.16	61.5
23445	110.29	87.9	82	231.61	62.42
18115	174.03	108.43	71	231.75	102.05
11429	189.45	42.84	72	232.42	40.03
11520	175.16	127.89	72	233.8	92.23
7927	202.04	106.05	70	234.79	57.37
22099	137.03	97.01	71	235.76	97.02
7888	376.09	171.23	72	236.43	56.75
17496	75.49	73.53	76	239.51	173.47
11742	161.82	79.25	71	239.68	82.64
6855	194.24	59.54	71	245.57	58.27
22928	87.17	110.53	70	245.88	162.18
7064	397.22	140.47	77	247.28	40.15
10879	202.31	103.86	70	248.56	66.82
20757	401.81	200.88	71	249.74	57.1
7113	200.31	111.11	74	250.23	78.75
11635	186.84	60.17	75	254.75	47.63
135	174.94	73.25	78	256.19	65.78

TABLE 3A: General Toxicity			Document Number 1650775		
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
24235	390.14	159.67	70	259.52	50.47
1479	205.28	61.98	72	261.61	51.03
5923	172.52	80.09	78	262.06	70.65
15642	368.73	123.22	77	262.87	41.31
9336	140.36	75.51	72	264.38	147.6
23325	326.83	125.56	70	265.55	63.28
9063	214.94	71.54	74	266.92	47.88
23612	382.82	255.62	72	267.25	92.93
912	326.5	67.38	73	268	33.47
14506	208.78	65.03	70	272.49	69.62
5748	328.41	66.67	70	274.63	44.97
8477	399.36	174.12	71	275.64	90.8
11021	177.75	93.53	73	275.95	97.97
8630	206.38	87.63	72	276.18	71.7
12331	142.97	91.35	73	276.42	113.01
12694	196.38	106.12	70	280.6	91.59
23380	201.35	91.04	71	280.63	98.56
25747	406.23	174.62	79	281.96	48.12
3418	416.76	178.28	75	282.48	51.77
19298	475.37	243.42	71	283.29	78.74
23558	187.58	94.53	72	284.57	75.57
6366	365.38	251.12	70	289.81	76.83
14103	153.89	84.24	76	291.22	113.41
24219	410.88	138.62	75	297.66	69
1929	232.96	81.98	71	298.56	77.17
5863	225.48	130.42	75	299.73	84.35
3504	395.85	157.69	70	301.1	58.36
4868	220.65	100.78	75	301.7	70.8
1753	235.94	62.13	72	304.05	74.62
22679	185.35	110.73	72	304.26	119.66
23230	431.68	274.8	77	305.51	73.66
17401	211.41	101.33	70	308.15	101.7
4179	444.58	228.79	73	308.58	63.03
24645	228.44	65.97	73	308.66	90.32
19679	212.7	94.25	74	309.08	79.13
8387	209.62	77.78	74	309.81	64.43
17324	236.31	65.13	73	311.13	52.23
1501	434.85	171.45	79	314.29	63.39
22582	224.5	87.58	71	316.36	75.3
25702	423.41	113.7	72	320.39	51.32
9399	222.67	63.69	76	320.67	86.48
3131	228.57	86.2	72	321.25	92.07
812	231.65	67.37	76	321.96	51.58
15519	303.98	284.36	71	322.04	142.67

TABLE 3A: General Toxicity					Document Number 1650775
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
1409	258.93	68.93	72	323.5	60.85
17049	207.81	93.01	77	324.1	63.71
7003	213.89	133.94	75	328.74	101.01
15612	208.41	106.4	71	329.06	202.57
851	259.03	53.32	76	331.68	47.82
4291	203.94	139.04	77	334.29	127.4
1478	262.27	68.1	74	334.41	51.89
7868	201.78	131.72	80	338.05	94.52
19469	284.04	59.16	72	342.98	50.36
15700	259.03	65.96	77	345.34	50.31
15197	263	83.78	70	348.89	85.31
2484	152.64	144.08	75	349.45	189.22
21396	274.52	76.97	73	354.24	57.86
15032	262.98	104.76	72	354.96	94.2
6825	321.55	146.79	71	355.67	98.41
14767	212.27	97.6	80	359.19	95.6
15136	482.9	133.86	71	361.06	68.44
2993	498.11	173.18	73	362.5	53.1
1175	211.25	155.83	72	367.03	107.25
16680	296.57	157.31	71	368.4	135.7
961	300.69	83.8	73	370.86	65.28
2696	463.19	111.26	71	371.94	59.78
17256	266.11	96.28	72	373.05	70.36
4937	305.59	112.68	74	375.59	89.26
18860	314.98	128.88	70	375.92	92.09
23884	312.54	72.12	70	379.68	59.35
17850	516.17	220.77	70	383.69	72.82
17175	504.94	132.64	72	384.43	64.15
12946	275.06	103.13	74	384.61	80.84
23322	308.64	91.46	73	385.69	58.02
16327	318.14	112.83	72	386.27	63.57
6824	820.58	540.91	70	386.87	102.09
1900	230.35	153.17	72	387.22	135.44
14869	290.26	114.01	70	388.39	93.33
15239	472.89	104.14	70	393.48	56.96
20694	256	155.8	75	396.34	127.36
6321	661.68	352.96	71	397.84	101.24
21157	628.44	255.63	70	401.01	132.71
1529	316.33	75.8	73	401.61	56.86
5934	166.87	133.41	76	401.67	162.84
18597	452.56	154.66	72	402.92	64.14
6801	284.93	123.62	70	403.58	114.82
8317	302.02	115.59	71	403.7	92.47
3959	651.41	284.48	73	404.94	125.39

TABLE 3A: General Toxicity						Document Number 1650775
GLGC ID	Tox Mean	Tox StdDev	LDA Score	Non Tox Mean	Non Tox StdDev	
6017	218.37	162.51	71	408.35	157.64	
7785	309.16	154.16	71	411.11	92.69	
18453	272.77	135.91	72	412.12	103.91	
11157	347.22	111.72	73	412.71	76.32	
2799	186.49	165.24	73	413.66	193.94	
18606	551.54	140.45	71	415.6	65.98	
25480	298.56	93.25	80	417.76	62.1	
6554	327.78	86.42	75	418.15	72.16	
22395	337.48	106	70	424.15	101.1	
18861	353.52	146.94	71	431.18	96.34	
556	363.95	72.87	72	431.39	47.74	
15016	614.84	191.45	72	431.42	106	
20707	297.52	182.87	72	432.6	110.59	
6615	313.91	151.88	70	435.29	105.91	
25675	559.03	149.18	71	435.84	78.46	
24458	391.59	66.22	70	440.47	58.22	
2264	348.28	114.55	70	442.01	101.65	
811	339.77	83.76	80	442.46	54.75	
14962	595.24	186.44	71	443.26	86.3	
9905	351.99	86.2	73	443.66	62.13	
4670	1011.12	757.17	70	449.34	279.51	
15135	572.07	128.52	72	452.98	71.41	
1877	381.72	99.89	72	455.58	70.01	
2905	368.76	236.61	74	455.99	171.06	
10176	362.61	131.62	73	458.21	78.68	
8880	270.36	150.83	71	461.94	178.82	
21977	333.82	102.68	78	464.63	71.57	
19103	373.87	152.27	72	466.17	87.18	
2505	361.86	109.11	73	466.31	72.15	
7582	256.38	164.17	72	466.34	223.76	
18001	369.81	89.98	72	467.77	75.36	
15755	405.73	112.28	71	473.79	67.48	
24577	583.7	137.54	73	474.11	65.9	
20299	326.39	113.27	76	477.33	90.93	
7697	273.75	100.92	83	481.09	117.81	
18867	425.79	164.92	71	486.56	85.09	
16726	386.57	78.35	71	489.29	90.61	
18522	338.66	110.39	78	493.05	127.44	
794	364.93	131.6	73	493.86	73.31	
21097	596.6	213.78	72	494.87	76.63	
11166	392.77	163.68	74	496.16	102.35	
3823	819.94	253.21	84	496.62	131.46	
20701	546.93	267.9	71	497.17	122.04	
13283	374.45	137.36	71	498.65	90.97	

TABLE 3A: General Toxicity			Document Number 1650775		
GLGC ID	Tox Mean	Tox StdDev	LDA Score	Non Tox Mean	Non Tox StdDev
14312	379.02	130.24	70	498.8	162.03
1561	489.56	192.41	70	503.1	74.48
11693	280.1	210.45	74	504.39	202.02
19470	355.43	120.62	75	507.23	102.75
20705	406.75	228.32	72	520.73	125.68
6060	377.46	110.54	75	524.04	95.02
4143	411.36	153.04	70	526.83	142.72
573	397.93	141.77	74	527.31	101.53
2111	431.14	135.97	70	535.18	95.74
6132	389.97	132.3	70	536.05	116.38
1531	432.89	99.85	74	537.37	84.23
13684	732.21	234.57	71	538.64	123.03
4914	320.44	176.4	77	542.57	159.28
16172	384.09	149.87	71	543.43	107
18661	375.83	155.78	71	546.25	136.03
14035	354.4	185.79	72	546.44	215.25
18452	376.32	156.49	75	548.91	124.57
10109	683.1	154.88	71	554.69	60.26
15113	422.52	185.06	72	557.21	136.1
12087	426.39	140.52	70	558.91	91.57
11492	398.17	152.29	73	559.08	143.79
14083	400.42	184.48	74	569.39	131.38
23961	487.24	102.51	71	571.23	72.66
6761	734.58	239.42	73	572.66	144.55
16993	402.56	131.25	80	574.27	86.25
11536	347.49	123.19	77	575.39	198.99
12312	415.93	131.04	75	579.26	98.18
20810	686.37	181.4	70	589.89	79.84
24771	441.44	127.76	75	592.18	94.5
6007	477.65	139.01	76	592.68	113.45
3145	432.3	212.79	72	610.87	178.16
12064	392.31	195.73	78	611.49	148.58
15080	468.83	133	74	613.82	131.38
22338	858.3	334.36	70	633.42	176.07
23437	417.21	173.85	75	633.59	238.89
20397	775.65	145.47	74	638.29	86.47
22930	206.34	282.8	72	638.83	389.14
5943	365.28	277.04	78	658.15	266.99
13088	440.35	191.07	72	659.11	130.73
3969	461.16	167.2	73	671.43	138.26
2536	229.18	164.07	75	680.76	402.5
8946	488.94	198.29	74	698.4	191.02
1173	454.86	255.52	73	701.71	147.85
6613	475.14	319.24	71	703.21	206.38

TABLE 3A: General Toxicity			Document Number 1650775		
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
17847	587.34	146.42	73	728.57	116.89
19069	401.65	251.38	70	736.55	312.13
3121	582.17	314.22	75	743.82	177.43
2762	549.37	222.1	73	744.04	144.72
9191	353.85	236.51	80	747.6	226.01
17339	394.82	309.4	71	757.04	450.78
3365	465.6	196.26	75	759.09	201.02
5622	781.85	245.85	70	761.19	118.25
19729	390.13	332.32	78	764.27	355.89
9012	363.63	210.98	77	764.48	253.76
4193	592.69	173.22	72	771.85	108.77
8549	428.57	212.41	77	776.74	195.59
16190	633.77	300.61	71	788.33	198.05
6143	563.65	311.9	76	807.95	145.12
11228	611.37	254.64	71	817.25	249.82
19830	639.79	218.85	75	827.94	161.07
11504	659.77	278.75	70	831.93	222.74
2569	457.34	317.75	82	855.43	152.77
12160	812.82	573.26	70	864.88	230.19
21341	583.63	407.72	73	869.75	255.69
24321	471.3	256.45	83	871.6	204.88
14584	778.69	204.76	72	899.51	154.36
4440	592.51	190.31	81	903.2	141.99
17340	1192.58	780.31	70	918.51	258.08
2196	676.58	230.37	76	961.23	265.77
16879	875.19	424.83	74	998.63	195.4
14118	716.41	266.36	72	1006.89	263.75
20503	598.26	362.91	74	1021.64	320.28
12306	1122.58	844.77	71	1023.1	338.53
2911	675.36	278.69	72	1039.76	290.7
18796	825.55	557.51	70	1043.22	369.63
19732	639.42	377.16	74	1044.68	344.85
11205	763.23	299.36	72	1062.45	233.92
13634	1541.83	591.67	70	1065.68	230.26
8692	729.45	328.96	71	1075.69	284.09
22559	707.2	351.3	74	1078.43	298.05
9475	633.07	305.29	76	1091.11	321.49
6033	695.09	293.08	78	1093.71	230.15
7893	681.36	341.8	72	1123.77	299.15
3822	1790.91	546.55	78	1156.91	279.92
18910	691.91	316.7	77	1158.26	375.48
16703	811.27	347.36	78	1176.58	244.51
10984	769.03	347.66	74	1177.95	295.11
24162	935.19	218.55	71	1183.5	254.36

TABLE 3A: General Toxicity

Document Number 1650775

GLGC ID	Tox Mean	Tox StdDev	LDA Score	Non Tox Mean	Non Tox StdDev
14960	1815.81	619.16	72	1189.85	282.97
22368	809.54	304.72	78	1204.44	255.44
14512	758.14	344.89	75	1207.73	316.98
22929	345.04	524.79	76	1263.79	749.31
6633	1158.38	523.64	70	1282.41	230.42
5899	868.41	419.97	75	1320.55	275.91
17027	885.56	416.43	74	1334.54	460.45
633	1120.93	302.27	71	1460.55	215.38
15240	1096.17	411.07	71	1507.99	426.62
3916	981.26	439.68	78	1583.55	340.89
22554	987.76	444.02	77	1595.12	393.47
3995	1025.02	387.98	75	1611.33	356.12
16885	1112.24	354.14	71	1613.71	341.53
9889	981.18	477.47	73	1620.07	396.24
15029	925.54	487.41	79	1688.81	378.2
6015	1123.82	384.91	78	1698.32	346
4330	991.16	483.62	84	1718.02	326.97
18909	1097.68	570.79	73	1735.42	607.51
3934	1109.15	552.14	74	1739.43	460.08
19363	867.12	620.13	74	1779.39	738.12
18002	1288.49	485.23	71	1800.22	448.73
4933	1364.86	630.42	74	1830.55	501.46
6380	1372.29	707.55	71	1841.36	514.23
16883	1363.62	527.7	78	2010.57	420.12
6072	1574.16	580.37	71	2013.52	377.64
17812	1417.56	569.56	70	2054.51	507.28
16701	1417.08	583.17	75	2071.93	447.2
6016	1345.93	620.12	75	2194.85	585.99
23261	1440.1	757.17	76	2245.13	579.05
9016	1484.15	791.38	72	2570.48	765.58
17524	1867.91	789.56	72	2578.07	684.86
22558	2228.15	660.37	73	3099.17	679.05
20502	2254.47	1019.37	72	3293.47	799.82

TABLE 3B: Hepatitis-inducing and NSAIDS				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
1661	41.81	18.92	85%	1.48	29.99
16317	30.67	11.58	80%	8.6	15.46
11893	54.33	34.89	85%	10.78	84.99
1507	46.98	9	89%	15.22	15.58
22966	36.69	8.83	81%	19.74	17.28
19671	37.69	7.44	85%	22.27	14.65
20016	36	8.96	81%	22.47	17.54
18495	49.47	12.55	87%	26.89	16.39
671	1.28	14.77	83%	29.18	22.7
1221	443.26	150.05	94%	31.23	89.26
25938	56.45	7.66	83%	32.22	17.92
18389	86.77	18.28	87%	33.41	32.92
11974	-0.81	15.18	84%	37.19	30.74
15834	-27.94	45.21	80%	40.53	65.46
20161	128.51	48.18	89%	43.77	57.9
17809	73.73	16.32	83%	46.32	27.65
7056	3.07	13.95	81%	47.6	27.96
5384	140.18	41.23	89%	47.78	62.23
16809	124.52	30.87	89%	53.12	26.62
11423	97.3	21.17	90%	54.32	20.04
22918	25.37	5.71	92%	57.72	29.27
20354	223.3	84.74	94%	65.21	49.13
18529	131.4	33.67	86%	68.42	53.24
1514	90.15	14.51	83%	70.26	23.25
8079	-4.51	23.75	93%	71.3	43.24
23847	116.7	16.84	84%	72.04	35.87
9712	23.03	12.25	88%	77.04	28.42
3660	16.83	21.57	82%	79.66	62.38
11904	167.34	25.7	93%	81.27	36.83
19158	45.35	20.66	81%	83.61	36.03
3710	-36.33	22.78	94%	85.53	112.55
15207	201.4	59.51	87%	87.46	53.13
18272	60.07	14.42	82%	88.02	33.03
353	141.35	40.91	85%	91.87	108.42
19410	151.13	23.55	87%	95.16	23.41
22321	170.96	42.18	92%	100.6	89.13
17277	197.62	54.02	87%	107.61	40.04
8597	164.65	22.23	88%	114.16	40.18
22151	53.9	21.51	85%	114.65	59.1
8274	76.86	17.29	87%	123.17	47.02
6532	271.93	51.51	94%	134.9	41.19
21570	190.77	30.4	81%	139.02	39.64
2555	331.4	107.66	92%	140.78	56.13
25370	84.18	22.52	80%	142.29	76.05

TABLE 3B: Hepatitis-Inducing and NSAIDS

Document Number 1650775

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
14208	94.74	20.59	84%	147.42	57.13
4250	206.6	31.57	81%	151.25	44.71
1521	259.23	49.47	85%	156.72	61.63
19075	223.09	35.39	81%	163.86	101.01
23584	77.34	44.36	81%	169.97	88.21
23855	348.59	60.39	85%	174.64	78.04
9595	340.35	75.95	82%	175.69	67.44
13332	103.75	23.14	88%	187.8	61.54
10544	215.74	17.73	83%	188.96	55.01
20914	95.15	42	80%	195.52	132.48
1796	121.33	29.79	82%	209	97.51
21039	106.61	32.3	84%	211.38	102.32
18891	79.72	50.3	84%	246.65	190.37
5464	135.66	32.82	82%	247.44	149.05
15786	143.55	47.13	84%	247.54	88.85
22619	538.26	124.75	87%	252.1	119.33
2655	82.89	32.9	90%	258.6	179.08
12156	181.92	29.95	83%	278.7	159.97
17664	741.68	141.39	92%	307.07	186.68
3504	500.63	92.33	90%	315.63	104.18
21281	205.42	64.7	81%	330.89	91.63
23890	215.59	58.3	82%	335.94	112.79
21663	239	51.32	81%	340.75	88.67
1795	160.6	58.49	90%	341.81	148.58
6825	186.43	50.61	90%	343.11	120.89
1900	172.64	60.15	81%	346.3	165.46
18465	620.04	89.19	89%	351.76	235.3
19412	785.76	148.65	93%	362.14	121.09
4026	890.4	293.19	94%	365.48	125.1
9148	247.98	44.83	82%	370.2	91.6
12928	537.35	88.04	83%	411.28	98.02
2905	272.3	68.62	83%	428.13	203.06
21657	770.91	200.72	85%	465.93	129.71
15127	328.43	46.16	84%	473.84	141.3
20701	957.82	322.59	85%	491.66	156.52
23125	211.15	54.99	87%	522.67	517.03
15606	391.12	82.13	80%	555.3	143.44
13557	380.72	110.05	84%	601.18	180.33
3365	412.07	116.59	83%	652.4	245.48
18890	249.81	125.41	88%	681.61	362.92
21740	1634.89	574.14	94%	692.6	269.8
3121	283.35	133.91	89%	701.53	256.63
16458	914	77.34	87%	721.93	196.36
11720	1413.34	300.55	94%	727.31	251.26

TABLE 3B: Hepatitis-inducing and NSAIDS

Document Number 1650775

GLGC ID	Group Mean	Group StdDev	LDA Score	Non Group Mean	Non Group StdDev
11504	489.83	118.52	82%	806.57	268.81
17768	607.41	128.96	82%	831.34	168.24
13093	311.95	133.36	85%	873.19	562.27
6236	496.56	151.3	84%	902.06	432.96
23449	168.69	130.37	84%	927.26	659.99
23989	1753.97	311.2	89%	1058.6	400.01
23448	180.53	167.78	84%	1073.75	757.46
24289	653.83	137.29	88%	1100.08	340.79
16885	781.13	224.04	92%	1490.2	403.55
3917	948.73	233.94	87%	1606.37	494.39
6072	1216.55	290.18	86%	1863.45	506.08
9016	1131.05	452.13	84%	2271.36	942.23
6189	1001.77	624.81	84%	2994.32	1665.75
16884	1730.22	430.96	83%	3305.32	4446.34

TABLE 3C: Necrosis and Fatty Liver

Document Number 1650775

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
7271	47.32	123.63	82%	-98.96	40.35
1727	109.71	134.11	80%	-50.93	105.7
5780	186.95	173.5	86%	-46.09	31.81
13203	59.69	60.36	82%	-17.7	44.77
16513	26.79	31.17	82%	-17.26	20.41
14619	43.31	34.51	85%	2.15	12.76
4553	26.34	19.46	83%	3.22	9.94
13458	45.73	26.41	89%	5.65	18.85
1610	44.15	19.04	83%	12.68	16.79
14693	74.3	48.25	83%	13.17	17.15
23679	133.75	76.1	90%	13.54	19.85
20456	59.55	30.52	86%	15.2	27.25
5733	152.59	121.24	80%	16.96	49.09
23435	130.84	87.29	81%	21.19	45.23
15312	97.29	57.4	83%	23.69	24.18
23678	101.95	55.99	89%	23.69	13.19
15861	71.17	46.83	82%	24.47	42.1
9181	83.64	43.77	86%	24.64	15.48
1598	201.08	146.9	80%	25.42	45.83
19940	83.79	44.07	83%	25.73	17.82
9796	72.8	40.14	82%	25.76	21.99
16085	106.34	47.32	89%	28.48	22.62
13467	155.47	95.96	86%	30.98	34.92
16618	94.85	58.13	80%	33.73	25.67
24710	86.03	43.14	83%	33.9	21
23260	157.52	100.81	83%	37.65	37.29
22876	70.57	22.75	82%	37.66	16.34
9331	80.05	31.38	80%	38.03	18.65
12614	139.71	71.97	88%	39.91	23.39
3280	81.33	28.39	81%	40.1	20.81
13874	88.42	37.45	84%	40.85	22.09
15862	84.57	34.63	80%	42.44	41.06
5926	80.04	27.03	83%	42.65	20.36
20449	254.92	200.63	82%	44.06	38.62
15313	148.78	79.95	82%	44.12	32.74
2897	110.58	50.4	86%	47.14	25.32
10549	203.78	148.01	82%	49.51	39.18
7243	132.31	62.02	80%	50.65	27.72
14939	115.22	49.92	83%	53.09	45.97
14242	118.61	49.19	85%	53.41	25.56
7161	136.07	72.13	81%	53.54	28.94
20708	91.32	26.75	86%	53.6	18.5
3831	104.66	45.67	83%	54.97	24.3
21707	135.19	53.83	81%	55.69	51.38

TABLE 3C: Necrosis and Fatty Liver

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
19264	117.33	44.24	83%	59.31	20.88
19150	109.31	32.72	86%	60.72	15.98
17687	99.1	21.62	85%	61.04	15.35
14462	156.22	62.83	84%	62.47	36.02
7036	131.87	57.57	81%	62.54	25.28
11527	177.9	80.35	84%	62.69	44.14
20082	124.7	51.02	84%	63.08	42.14
17736	432.83	313.35	81%	65.71	142.15
1841	136.63	50.08	81%	67.1	44.8
20523	102.48	38.3	83%	67.66	66.06
12965	169.8	78.23	83%	71.26	51.46
6085	208.53	104.4	83%	72.61	45.7
14458	330.83	217.41	83%	73.29	65.46
24236	184.01	75.75	85%	73.32	33.88
23160	176.55	75.81	83%	73.36	35.73
13251	323.03	180.5	84%	75.07	50.76
9784	153.22	64.68	82%	79.16	35.89
15398	239.17	147.09	84%	79.65	55.81
353	280.56	162.02	81%	80.59	90.86
20684	131.06	32.29	86%	86.62	20.64
14258	198.53	76.19	81%	87.06	38.11
22877	194.7	70.48	86%	93.61	36.71
1411	202.73	82.72	81%	98.83	39.17
11660	170.21	44.78	84%	99.62	34.3
23099	201.64	75.74	81%	104.62	41.86
23438	195.84	62.14	85%	104.93	43.18
17734	614.42	397.11	81%	110.47	174.81
7063	256.37	132.72	84%	114.31	69.93
1399	215.1	91.12	82%	116.84	76.67
5008	201.49	60.1	84%	118.38	36.13
11331	223.98	89.07	83%	120.5	40.92
25257	274.45	132.38	80%	121.28	48.13
16321	210.67	63.57	83%	124.13	43.97
20891	244.46	85.07	84%	125.01	52.71
2938	92.66	29.87	81%	127.24	29.13
22038	251.93	88.6	85%	127.34	44.31
17369	207.5	75.1	82%	129.13	60.27
5794	226.31	75.22	81%	130.44	40.81
5489	273.17	111.54	82%	136.39	59.55
20843	213.04	53.39	82%	136.57	33.06
2555	219.93	71.85	81%	139.38	59
15374	243.38	59.14	83%	141.32	44.16
24388	624.21	327.48	89%	143.82	68.72
22432	292.49	109.98	83%	146.05	50.66

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
18418	239.91	82.99	83%	146.58	40.53
12999	347.57	138.68	83%	153.73	65.66
26369	308.75	109.91	81%	154.12	55.73
14051	299.77	104	82%	156.87	52.25
4592	257.24	62.73	86%	157.37	38.03
4952	684.4	441.82	80%	158.99	145.89
23184	332.9	137.24	81%	159.3	52.72
7887	338.64	115.83	86%	162.05	60.73
18755	279.19	80.05	83%	163.56	53.86
17735	512.06	294.56	82%	167.32	151.69
4781	344.83	111.41	85%	169.37	65.78
22197	414.63	204.11	83%	169.48	88.02
23855	282.27	93.29	80%	171.07	75.56
14224	333.11	104.73	83%	174.8	67.56
6796	410.28	172.66	86%	185.7	72.52
20735	408.72	201.02	82%	185.89	74.3
21696	297.51	89.84	81%	186.09	42.02
11561	362.43	142.46	82%	188.78	64.86
3203	308.57	101.34	81%	194.76	46.19
7414	535.61	335.02	83%	197.35	92.11
15900	420.93	177.15	81%	202.45	80.18
23299	835.51	456.01	87%	214.06	131.12
2615	386.6	100.97	86%	217.6	65.98
5867	511.55	202.2	82%	233.57	78.63
24597	382.02	100.07	86%	233.91	54.34
11404	578.06	245.72	83%	238.77	146.51
1460	401.14	112.53	84%	244.96	91.82
498	416.48	120.92	83%	249.32	96.83
16859	472.45	162.72	81%	251.02	122.56
7888	537.76	182.29	85%	257.15	89.71
16756	553.61	229.09	83%	281.56	137.56
7064	502.34	176.81	85%	282.57	116.55
3418	612.35	201.12	86%	297.77	79.32
21458	1369.61	969.19	80%	306.95	224.17
2818	499.79	119.08	85%	321.5	81.64
23120	466.17	110.7	82%	322.94	76.21
4179	559.24	157.01	86%	323.2	127.86
21672	477.65	79.51	85%	327.31	77.78
23229	626.51	235.94	81%	338.12	95.94
1501	526.15	137.21	81%	342.01	115.25
7785	234.09	120.53	83%	402.39	211.3
6824	1330.86	651	84%	457.47	265.81
14962	735.07	188.78	85%	460.88	120.76
13646	647.84	120.93	81%	469.35	113.75

TABLE 3C: Necrosis and Fatty Liver					Document Number 1650775
GLGC ID	Group Mean	Group StdDev	LDA Score	Non-Group Mean	Non-Group StdDev
11693	194.51	110.15	81%	475.41	349.8
6132	303.54	124.75	81%	496.77	136.48
7935	319.95	130.18	81%	539.48	150.81
4193	471.49	196.67	86%	732.69	138.33
2569	363.05	288.34	84%	741.53	276.55
6143	440.17	239.99	82%	761.21	219.76
20503	406.67	194.67	86%	913.12	368.79
16703	657.32	260.25	82%	1074.26	319.63
7403	747.37	603.65	82%	1275.15	420.96
7199	888.57	501.29	81%	1460.27	432.28
15029	731.54	467.45	85%	1526.56	513.26
4330	744.46	374.66	83%	1547.62	486.62
6380	907.19	397.41	84%	1723.63	601.93
16883	1078.56	580.73	82%	1877.14	516.54
6016	1048.32	457.34	84%	2002.18	710.82
23261	1133.22	790.5	81%	2083.71	702.84
9016	1179.45	473.8	81%	2319.89	929.08

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TABLE 3D: Necrosis With or Without Fatty Liver

Document Number 1650775

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
5780	149.44	174.82	83%	-46.61	31.66
14619	39.67	32.26	81%	1.81	12.49
5504	40.54	56.94	82%	4.45	12.06
13458	39.01	28.21	82%	5.58	18.92
15860	31.78	22.42	81%	6.3	24.49
14693	68.27	45.68	82%	12.72	16.78
23679	113.2	81.03	82%	13.37	19.88
15312	89.9	55.01	81%	23.16	23.77
15861	75.5	43.95	86%	23.4	41.45
9181	78.27	41.53	85%	24.18	14.99
16085	90.49	54.22	81%	28.58	22.73
13723	125.68	115.97	84%	29.26	45.67
23260	150.76	92.71	85%	36.36	35.87
9331	78.82	28.75	82%	37.48	18.21
12614	122.76	74.47	81%	39.76	23.36
13874	91.42	39.76	85%	39.87	20
15862	87.12	32.75	83%	41.59	40.71
2838	145.55	92.3	83%	42.77	33.6
15313	138.73	76.22	81%	43.33	32.1
2897	102.26	48.95	80%	46.84	25.34
10549	187.81	138.33	82%	48.44	38.17
14939	109.91	48.48	81%	52.56	45.94
14242	115.77	46.52	85%	52.64	24.7
17736	447.8	300.15	85%	58.86	128.94
19264	110.15	43.15	81%	59.01	20.79
14462	146.65	60.75	83%	61.81	35.78
15663	150.74	81.27	81%	61.88	28.94
13251	296.06	174.05	83%	73.46	48.79
6012	176.64	72.48	83%	84.55	40.71
22877	181.18	70.29	80%	93.15	36.67
1411	191.96	79.06	80%	98.12	38.82
11660	165	42.53	82%	98.96	34.06
17734	628.16	382.62	85%	101.62	156.16
6820	162.7	43.24	81%	105.26	24.87
1399	254.19	123.38	83%	112.16	66.1
7063	246.94	123.92	84%	112.9	69.1
24375	284.9	130.19	82%	122.22	50.94
22038	242.92	82.73	85%	126.16	43.47
15282	345.28	174.2	83%	133.39	77.83
20843	205.85	51.68	80%	135.98	32.8
11235	307.17	131.67	83%	138.32	42.12
15374	245.25	54.33	85%	139.6	42.14
8886	258.45	90.02	82%	140.07	40.87
24388	550.6	333.76	85%	142.43	67.72

TABLE 3D: Necrosis With or Without Fatty Liver

Document Number 1650775

GLGC ID	Group Mean	Group Stdev	LDA Score	Non-Group Mean	Non-Group Stdev
6039	298.35	118.74	82%	149.78	54.28
26369	303.77	102.86	83%	152.16	53.29
14051	288.38	98.7	81%	155.61	51.3
4592	241.58	65.95	80%	157.11	38.16
17735	549.36	298.48	85%	159	133.2
7887	321.75	114.32	83%	160.72	59.56
18755	284.26	77.14	85%	161.37	50.75
4781	337.58	103.44	85%	167.27	63.76
20735	413.37	184.38	86%	182.1	67.45
7414	505.45	309.7	84%	194.61	89.53
11403	734.85	335.38	87%	196.39	177.82
15900	425.49	161.92	84%	198.73	74.48
15543	413.52	162.64	83%	212.02	73.08
23445	63.7	78.02	82%	213.22	89.74
6911	135.77	67.21	81%	214.68	51.49
11404	616.53	242.57	86%	230.44	130.03
5867	485.57	189.97	84%	231.42	77.22
1460	416.34	113.77	87%	241.33	86.89
7888	525.74	174.65	87%	253.82	84.82
26123	592.58	263.62	81%	267.76	130.29
16756	536.74	209.62	86%	278.76	136.63
24235	489.44	179.4	82%	280.21	94.54
3418	575.64	197.63	85%	295.93	78.26
19298	630.43	229.07	82%	317.49	143.34
23120	479.07	107.1	84%	319.7	71.63
2818	482.71	116.97	82%	320.15	81.06
15700	230.09	67.32	81%	324.4	64.93
228	236.54	61.87	80%	334.29	69.66
15032	205.99	56.82	80%	339.35	104.9
13294	644.35	170.98	82%	387.09	129.3
20707	228.73	113.6	81%	399.4	144.8
20299	283.13	98.83	81%	438.73	122.19
6824	1346.97	605.91	87%	442.76	235.61
14962	719.5	177.74	85%	457.94	118.72
794	301.18	105.82	81%	460.38	105.58
13646	650.4	113.01	84%	466.4	111.75
15135	628.19	146.12	81%	475.33	93.64
11693	181.61	105.42	82%	480.77	349.7
23390	900.94	286.52	82%	482.87	204.25
6132	287.11	119.69	84%	501.07	132.83
20705	268.91	129.82	81%	501.83	170.59
16518	745.69	208.61	80%	522.4	147.11
24501	924.14	324.29	81%	549.2	118.31
13684	940.24	251.12	84%	561.02	160.11

TABLE 3D: Necrosis With or Without Fatty Liver					Document Number 1650775
GLGC ID	Group Mean	Group StdDev	LDA Score	Non Group Mean	Non Group StdDev
23961	413.97	100.86	81%	563.48	84.42
2350	914.43	280.02	83%	566.27	157.14
7262	1171.93	460.29	82%	616.91	222.19
15283	1210.53	436.26	84%	630.12	224.34
4193	484.87	182.86	85%	735.61	136.93
15365	1249.48	437.43	82%	780.82	1098.83
24321	376.06	230.84	83%	789.46	268.88
22559	540.14	342.39	81%	1011.15	343.11
5899	694.24	374.16	80%	1263.41	404.09
7403	704.59	553.96	83%	1286.73	413.15
7199	835.65	469.87	84%	1473.34	421.86
15029	702.04	429.52	87%	1541.16	503.02
4330	675.9	370.63	85%	1565.51	467.91
18002	948.21	459.72	81%	1684.6	511.86
6380	882.65	369.95	86%	1738.14	594.45
16883	1007.86	547.7	85%	1895.14	498.99
6016	963.32	454.45	86%	2023.72	694.11
23261	1077.62	726.72	85%	2102.8	690.37
9016	1096.76	480.03	84%	2344.1	914.36
3062	1684.88	888.35	81%	2819.77	870.18

TABLE 3E: Protein Adduct Formers				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
26190	48.28	140.35	73%	-116.76	71.12
8700	49.85	77.95	72%	-12.19	36.84
1661	36.36	40.61	72%	1.43	29.6
18323	56.4	33.89	74%	6.38	36.18
4348	50.39	34.87	73%	11.17	31.72
17481	36.46	27.96	72%	13.35	33.51
5434	29.26	14.26	76%	13.66	16.78
5930	23.92	9.03	70%	17.21	18.45
15778	24.37	10.62	70%	18.73	13.8
16251	28.52	7.89	78%	20.02	13.7
23315	33.84	16.8	71%	20.08	11.03
23843	65.54	53.1	73%	20.76	16.77
24268	31.94	6.01	72%	20.84	19.94
12185	40.45	26.74	73%	21.92	18.47
6026	60.83	27.25	80%	21.94	33.9
9603	38.75	22.25	71%	21.97	31.16
17747	8.38	6.53	74%	22.43	16.15
21799	-5.84	13.09	81%	23.01	22.31
14195	36.74	19.21	73%	23.09	19.24
3976	17.49	10.74	71%	23.34	30.4
6533	32.77	10.84	73%	23.83	29.19
9166	69.93	53.74	72%	26.99	17.75
4610	63.26	38.33	71%	31.07	36.11
16167	26.11	7.76	73%	34.04	13.5
13967	69.09	21.43	77%	35.02	22.23
17677	-27.82	68.69	74%	36.4	69.93
14449	56.08	25.32	70%	37.77	22.83
11700	55.37	19.55	71%	38.12	21.59
1538	7.74	23.48	75%	38.59	30.39
14053	24.71	9.07	76%	39.07	22.35
6804	17.85	7.18	72%	40.39	128.09
15834	-16.44	51.96	73%	40.56	65.53
23170	43.49	9.26	75%	40.79	23.99
21823	40.81	9.62	70%	41.44	26.15
11485	76.43	21.72	79%	41.78	31.48
26288	55.27	10.43	70%	42.31	15.42
25409	8.36	31.39	76%	43.05	24.65
15251	38.39	9.43	76%	46.23	24.25
8124	57.68	9.64	72%	46.93	19.16
14126	34.95	11.94	71%	47.89	50.38
25203	29.38	13.58	73%	47.94	21.85
9432	100.75	48.6	73%	48.25	28.18
2153	74.75	38.6	74%	49.01	17.57
11127	51.39	6.96	73%	50.24	17.35

TABLE 3E: Protein Adduct Formers

Document Number 1650775

GLGC ID	Group Mean	Group StdDev	LDA Score	Non Group Mean	Non Group StdDev
2933	50.64	8.95	72%	51.06	22.58
25615	71.69	18.81	70%	52.1	17.72
24654	81.41	24.85	75%	52.19	24.88
15018	84.77	83.88	71%	52.26	40.53
21707	126.24	73.39	70%	59.01	53.51
13918	98.73	44.7	74%	59.06	31.3
10549	42.34	9.93	70%	59.31	64.81
22566	92.71	49.39	70%	60.91	42.33
23304	84.45	28.37	70%	61.03	41.36
25413	37.94	16.74	79%	61.59	20.66
25410	30.99	21.26	78%	62.85	30.41
25411	27.66	23.64	80%	62.98	33.69
13581	83.19	33.57	71%	63.07	26.31
13932	-7.5	82.93	71%	63.9	55.62
14171	74.42	21.1	71%	64.55	37.62
90	36.07	18.79	70%	65.79	40.02
17257	114.03	67.46	70%	67.08	34.52
7537	58.32	14.12	77%	67.47	33.14
25397	33.74	21.21	73%	68.15	31.21
17894	82.35	13.84	78%	68.79	26.36
6814	89.6	32.08	73%	69.88	23.93
21893	44.34	8.05	72%	71.05	72.75
11438	111.77	49.88	74%	71.31	27.16
23324	87.26	41.21	73%	73.64	76.07
4168	104.37	21.68	75%	75.31	30.27
7903	30.15	21.43	74%	75.81	76.12
14335	83.34	14.3	71%	76.03	33.52
24589	112.98	48.88	76%	76.16	48.86
9712	59.65	43.73	73%	76.42	28.63
20980	95.23	16.77	71%	79.04	22.6
6003	97.63	17.55	73%	80.11	26.51
13175	132.4	51.99	72%	81.55	39.28
19315	140.15	42.44	84%	81.73	41.23
15156	110.09	19.69	72%	81.74	31.08
1169	63.7	12.97	72%	82.79	31.48
6032	51.63	16.54	72%	83.57	48.94
17400	145.45	66.75	71%	85.87	52.06
2006	25.42	45.67	71%	86.52	90.27
21068	264.69	160.27	72%	87.31	146.99
11215	-7.35	163.64	72%	87.87	83.21
3074	54.49	18.32	70%	88.91	83.5
22961	111.83	20.67	72%	89.09	31.98
2506	141.66	97.88	71%	91.9	70.92
6409	148.77	36.6	74%	92.24	57.46

TABLE 3E: Protein Adduct Formers					Document Number 1650775
GLGC ID	Group Mean	Group Stddev	LDA Score	Non Group Mean	Non Group Stddev
22531	91.66	12.53	73%	93.27	36.37
21209	227.02	212.22	71%	95.2	92.15
2383	83.79	16.73	73%	102.14	37.31
11174	184.12	65.2	77%	102.16	98.46
17368	171.8	96.78	71%	103.87	47.72
20851	137.3	28.16	71%	104.02	55.43
3091	153.51	67.82	75%	104.92	90.83
18390	78.71	19.55	74%	106.46	50.88
3073	52.19	23.11	73%	106.62	118.05
6798	135.78	43.18	74%	106.64	46.11
14600	214.24	98.46	78%	109.92	74.91
17617	99.3	12.59	72%	110.02	31.44
14638	87.23	22.1	77%	111.45	74.07
10184	123.58	33.76	72%	112.37	55.43
9170	183.59	55.27	70%	114.2	52.72
22151	79.59	31.13	71%	114.31	59.46
12880	139.94	22.05	75%	114.56	32.47
14937	131.42	66.88	72%	114.75	41.55
2342	166.44	44.77	70%	115.31	58.59
18612	131.39	23.5	75%	116.94	56.6
11691	62.73	41.24	71%	118	79.85
17451	101.96	15.77	72%	120.36	30.67
19566	145.76	30.8	71%	120.45	44.75
24508	154.79	40.91	71%	123.72	32.09
1641	165.12	40.83	70%	128.2	35.55
23885	161.49	29.33	72%	129.48	47.42
20930	134.38	23.9	71%	130.09	61.62
5795	132.03	27.82	71%	130.17	53.46
22051	101.35	28.02	72%	130.68	67.38
26368	145.81	51.6	71%	132.19	91.73
19605	113.2	19.79	72%	133.82	51.82
21040	-18.07	52.54	71%	133.85	229.8
14776	102.58	34.94	70%	134.24	48.08
1223	182.79	51.88	71%	136.08	48.54
13762	158.63	98.43	77%	138.6	59.12
11048	119.54	22.24	73%	142.6	56.03
2292	84.06	42.12	70%	143.71	71.66
17844	277.9	176.64	73%	144.36	79.81
12215	204	107.83	71%	146.76	116.15
2043	179.12	22.45	78%	147.6	36.11
4157	177.19	33.3	74%	147.73	62.63
20711	228.01	78.2	72%	150.83	116.07
26088	145.54	50.27	74%	156.38	187.59
17572	159.65	44.25	71%	158.21	87.38

TABLE 3E: Protein Adduct Formers					Document Number 1650775
GLGC ID	Group Mean	Group StdDev	LDA Score	Non Group Mean	Non Group StdDev
1690	229.65	95.98	71%	160.28	60.57
15141	173.57	16.39	73%	162.21	36.81
16700	83.29	55.96	71%	162.48	108.7
20380	146.38	29.01	71%	163.02	57.5
15959	167.27	18.31	73%	166.48	70.66
9598	288.09	95.08	73%	168.1	93.9
11590	190.23	28.5	74%	168.24	68.73
22806	131.95	29.2	75%	169.43	77.82
18588	206.23	40.15	73%	170.98	65.63
1141	203.77	31.9	74%	172.68	35.21
9595	271.77	94.28	73%	176.57	69.08
24146	216.8	34.19	71%	177.31	65.74
17291	239.96	109.02	74%	177.33	137.8
21717	206.89	32.09	71%	189.62	69.87
13640	218.18	27.37	72%	190.6	71.83
14007	153.67	25.25	74%	191.38	72.77
16562	238.09	59.35	70%	194.57	50.93
10187	223.84	49.38	72%	198.22	88
25802	244.19	49.71	70%	214.98	65.34
11742	217.52	133.21	72%	216.12	86.16
5020	191.66	26.95	72%	222.98	53.97
22603	221.37	90.45	71%	229.9	65.5
1728	238.87	23.07	75%	230.92	67.51
13534	182.27	33.55	75%	232.74	85.78
2868	286.73	53.61	71%	234.2	69.67
14997	375.7	196	72%	235.84	152.48
5111	393.78	167.65	73%	236.27	143.66
20063	181.07	59.31	70%	236.39	97.14
16780	267.07	94.4	75%	242.2	64.47
23337	207.26	31.63	70%	243.84	91.24
19052	433.77	178.35	77%	253.21	91.88
22619	416.09	190.68	70%	253.69	121.24
6821	297.59	92.7	71%	255.52	167.53
17794	256.5	47.37	72%	259.54	87.89
5110	444.91	212.14	72%	270.46	106.82
4929	215.55	43.79	71%	270.62	101.5
23698	318.89	170.39	75%	278.46	123.55
10594	382.41	57.15	78%	291.69	58.26
6366	466.38	163.71	75%	301.16	141.67
5091	204.8	54.15	76%	305.72	121.65
12317	489.39	140.01	77%	306.86	86.66
15122	284.14	30.38	70%	308.23	65.78
2763	390	85.38	73%	308.26	88.64
20715	439.32	105.47	74%	310.12	180.07

TABLE 3E: Protein Adduct Formers

Document Number 1650775

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
25644	345.9	39.5	71%	314.7	121.98
1175	204.91	111.96	71%	321.32	143.78
24161	356.93	42.23	71%	327.71	79.09
18647	397.22	64.9	73%	330.24	91.79
21281	233.54	99.86	71%	330.78	91.46
4179	625.2	324.6	71%	330.92	127.34
43	237.61	86.82	75%	341.37	75.07
19458	364	43.15	72%	346.08	133.08
23128	313.06	51.91	71%	349.02	136.57
22412	366.89	96.19	71%	351.91	164.5
3143	483.63	141.06	72%	352.34	102.15
6801	355	56.71	70%	360.03	142.03
6066	431.59	75.6	72%	368.47	141.78
21575	432.67	63.41	73%	374.58	82.96
8317	421.43	158.85	72%	379.92	111.94
4371	507.88	124.44	71%	394.01	171.93
11157	373.15	134.06	70%	394.37	101.64
24296	481.18	92.3	72%	403.62	139.39
556	373.54	45.1	71%	408.23	71.6
13055	482.08	75.69	75%	411.9	164.09
8173	519.73	67.84	74%	419.47	110.06
3219	317.14	59.47	73%	426.13	99.03
16278	309.41	102.23	78%	429.92	164.15
23608	566.48	164.2	70%	431.27	241.18
25777	330.46	55.36	76%	441.54	130.73
18522	334.4	99.2	70%	443.31	151.76
6188	512.63	55.77	74%	448.02	139.04
794	333.35	131.81	72%	451.08	111.83
11693	254.85	149.73	72%	463	348.51
14312	397.8	81.06	71%	466.35	160.88
5339	852.55	606.3	72%	468.96	257.55
13646	546.37	100.3	71%	478.7	121.95
22534	444.69	49.89	76%	478.75	159.7
15121	635.12	147.29	73%	513.19	224.34
5038	398.62	86.39	71%	513.52	201.59
7916	483.75	53.88	76%	515.32	200.18
4759	421.47	104.72	71%	536.6	127.07
2339	519.32	64.43	73%	536.85	137.81
16947	444.15	113.82	74%	564.09	119.37
24707	469.06	76.22	77%	596.18	184.62
13557	472.83	125.45	74%	600	181.83
11322	781.82	176.95	71%	605.26	189.58
16623	815.06	113.69	75%	643.07	187.67
20397	756.19	106.73	71%	670.62	123.59

TABLE 3E Protein Adduct Formers

Document Number 1650775

GLGC ID	Group Mean	Group StdDev	LDA Score	Non Group Mean	Non Group StdDev
3121	513.81	224.23	72%	698	260.45
6673	697.31	124.67	71%	713.3	302.28
4193	655.24	191.97	71%	718.19	154.45
7552	709.86	131.78	73%	813.29	320.57
820	636.5	127.73	71%	821.94	204.55
19105	924.47	159.69	70%	829.48	236.56
16169	456.68	219.61	72%	862.69	796.4
20503	559	204.67	80%	889.74	380.31
6236	529.47	148.78	79%	903.06	433.66
16879	841.82	418.27	71%	946.87	285.04
17340	1644.38	815.75	74%	997.68	474.22
7451	1340.55	383.41	73%	1014.34	341.2
12306	1456.43	258.06	79%	1024.68	517.58
18905	880.62	169.73	78%	1175.6	278.99
17027	844.61	248.1	71%	1257.61	538.33
22554	997.94	184.01	86%	1359.91	523.26
26147	1510.64	528.64	72%	1410.78	338.29
9192	941.24	221.51	74%	1413.17	565.76
23243	872.48	380.03	72%	1417.04	675.7
16885	1012.98	320.39	72%	1487.91	407.92
15029	1042.74	622.16	70%	1488.18	539.06
4330	1083.48	398.15	72%	1508.27	516.11
22266	1415.56	499.05	71%	1514.02	441.93
18002	1259.73	300.25	77%	1637.82	545.26
4933	1137.93	526.28	71%	1700.05	608.74
21091	1307.31	329.46	70%	1706.98	564.25
6072	1518.7	338.39	72%	1859.25	511.2
17812	1406.92	373.38	70%	1884.53	608.25
17107	1929.94	1307.4	71%	2218.38	823.7
9016	1497.78	482.54	71%	2267.81	949.1
20846	2090.67	1066.14	76%	2478.45	898.34
22558	2580.09	1019.35	72%	2867.4	846.53
6189	1470.69	763.08	73%	2992.11	1673.91
11623	2359.03	1401.37	73%	3039.92	2772.61
16884	1876.68	541.26	76%	3308.78	4455.6
6018	1795.01	783.44	73%	3626.1	3303

TABLE 3F: ANIT

Document Number 1650775

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
22513	633.15	232.37	98%	-132.38	329.17
19388	29.83	17.06	91%	-25.03	31.57
72	49.9	30.74	90%	-17.96	34.45
489	86.15	31.02	99%	-11.18	21.72
11645	46.52	22.15	95%	-10.46	29.11
15003	103.65	34.94	91%	5.13	35.34
4318	23.26	6.71	91%	7.08	9.22
372	43.1	11.62	90%	10.4	12.2
14400	115.49	28.78	96%	12.11	47.49
15480	45.43	16.54	92%	12.38	8.62
22397	98.15	29.08	90%	18.38	61.47
23679	58.03	21.94	92%	20.39	39.25
10790	-79.79	34.37	91%	24	51.35
16006	71.89	13.1	93%	26.66	31.65
15701	115.07	45.82	92%	29.52	22.06
25052	170.78	53.79	98%	31.24	82.74
1221	221.03	65.82	92%	36.47	104.6
23945	98.4	22.42	91%	37.09	29.06
11608	68.37	11.81	92%	39.75	16.9
20741	140.96	42.97	91%	47.33	36.73
5384	110.15	33.33	91%	48.7	63.05
1809	660.39	204.87	91%	51.86	210.98
21088	88.49	15.38	90%	52.62	15.58
488	302.77	84.83	99%	55.29	40.85
20708	69.43	8.17	90%	55.72	21.17
11940	79.89	7.9	90%	56.21	16.71
6585	124.92	40.67	93%	56.76	84.64
15914	167.68	28.59	98%	58.06	29.32
1279	124.99	36.23	92%	60.16	22.09
22487	203.14	70.64	92%	66.54	38.82
17894	123.11	19.61	91%	68.4	25.56
2801	158.72	27.08	95%	68.44	49.17
14465	5.28	16.66	90%	70.62	29.14
15892	279.1	77.25	95%	73.2	79.81
7903	9.08	6.85	90%	75.62	75.73
20772	127.51	24.47	94%	79.34	26.84
11904	152.49	15.73	96%	81.95	37.81
23522	149.93	28.04	91%	84.93	35.96
14017	168.86	47.57	91%	94.1	25.48
23869	219.91	36.9	95%	98.3	110.47
14016	172.79	34.4	91%	101.88	27.02
23005	231.25	60.04	96%	102.75	100.99
24453	296.76	77.39	97%	107.86	52.64
23872	208.24	51.83	93%	110.93	125.84

TABLE 3F: ANIT

Document Number 1650775

GLGC ID	Group Mean	Group StdDev	LDA Score	Non Group Mean	Non Group StdDev
10016	224.63	64.84	91%	116.67	48.65
17590	228.93	49.97	90%	127.17	38.31
4944	218.13	56.11	93%	129.57	134.8
15002	208.14	35.44	90%	134.25	36.07
20529	372.92	69.59	93%	138.52	121.65
20849	259.34	55.56	91%	150.94	38.19
15141	216.05	18.73	91%	161.78	36.17
15089	428.71	94.42	90%	164.31	111.52
24779	-119.55	53.79	90%	169.39	275.44
7665	325.89	51.47	94%	171.6	94
12577	530.07	99.18	92%	176.81	126.07
3253	242.21	21.26	92%	177.78	42.54
25069	384.72	63.15	96%	181.27	147.24
23182	70.96	27.02	90%	182.67	82.66
19043	461.37	93.08	91%	184.16	86.52
23445	44.92	13.64	96%	204.01	96.17
22928	18.25	13.42	90%	205.31	168.08
15300	301.52	31.01	95%	208.5	106.84
19073	357.79	55.66	90%	215.38	51.37
24237	602.69	44.81	99%	219.11	138.4
1447	293.32	18.87	94%	221.41	41.58
16408	151.08	35.06	90%	254.15	84.03
23868	529.77	129.48	90%	266.34	657.93
24810	103	36.24	90%	273.16	90.15
5235	460.06	75.16	90%	286.43	79.01
2802	498.79	58.22	95%	287.5	90.87
25747	698.21	163.03	91%	318.26	115.19
2818	510.22	88.82	94%	330.07	92.39
5934	42.22	26	94%	342.34	187.09
1501	711.93	121.22	96%	348.6	117.83
15535	499.6	40.24	91%	391.06	75.12
5437	327.15	25.07	90%	409.5	102.21
12928	607.12	43.69	97%	411.1	97.29
4207	611.82	98.48	90%	440.38	323.23
20701	762.37	110.98	94%	496.87	170.59
1562	360.31	37.96	90%	504.85	111.39
6824	806.51	180.29	90%	506.91	368.25
20983	343.07	66.3	93%	516.16	120.95
13088	199.67	54	96%	593.92	183.67
6613	320.2	65.66	92%	626.43	272.37
25024	451.39	46.56	91%	661.12	185.97
8549	262.14	62.15	93%	665.65	258.33
4193	484.74	47.1	95%	719.76	154.17
2569	257.19	110.15	91%	724.41	288.37

TABLE 3F: ANIT

Document Number 1650775

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
7892	1166.36	244.14	92%	809.73	244.53
18900	1202.22	137.08	92%	830.76	217.68
16879	540.35	100.54	93%	949.72	286.7
475	635.1	94.59	92%	976.05	230.62
5899	704.5	125.15	92%	1227.29	427.31
3916	883.71	181.1	91%	1427.83	464.67
10378	2563.09	466.04	90%	1469.47	449.7
19363	372.52	212.88	90%	1539.84	830.44
6072	1270.16	177.57	91%	1859.03	508.9
20502	1504.84	383.84	91%	3017.48	1038.48

TABLE 3G: Late Acetaminophen					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
18028	62.86	12.89	98%	11.46	17.68
6151	41.98	5.06	97%	11.63	19.32
1394	46.55	7.94	98%	13.22	8.97
15701	104.85	30.26	98%	29.54	22.64
21586	129.12	22.29	98%	37.42	35.11
18099	74.54	10.03	98%	37.77	12.82
18990	191.58	50.21	98%	37.78	56
5492	154.99	36.3	98%	42.55	45.33
16958	152.1	24.97	99%	48.17	21.95
25892	5.84	14.89	97%	52.01	13.92
4281	8.04	4.69	97%	52.71	20.31
20817	552.74	204.49	99%	56.23	83.19
494	-58.87	15.28	99%	57.66	57
17091	221.12	37.22	99%	64.55	35.7
5493	201.07	32.69	98%	68.52	42.64
4650	257.12	41.99	98%	74.24	55.94
20818	387.65	157.18	99%	81.37	42.47
8356	191.89	39.3	98%	81.94	31.64
17090	166.91	23.91	98%	82.55	25.23
6153	47.01	7.23	98%	89.68	30.74
1399	422.27	102.52	97%	118.53	72.23
18369	14.78	33.12	98%	154.92	43.99
8107	82.52	12.58	99%	157.67	30.22
21305	78.03	11.47	97%	162.22	42.69
16219	91.23	10.22	97%	162.24	35.05
20380	51.46	16.74	97%	164.24	55.84
14970	64.35	7.2	98%	165.35	37.88
11039	22.92	14.76	98%	165.75	75.12
1644	69.04	14.22	99%	166.93	43.07
25632	23.75	9.64	100%	170.77	437.48
25069	648.62	107.28	98%	177.18	137.77
12848	77.84	12.22	98%	178.82	51.97
15571	37.5	7.71	100%	182.36	613.17
5998	82.64	16	98%	198.22	47.74
1542	75.63	15.75	97%	201.9	67.93
11429	113.75	15.07	97%	220.8	45.17
11635	84.37	10.31	100%	235.11	58.7
24246	680.67	154.62	97%	235.68	110.38
17684	115.68	11.83	97%	243.52	58.44
1479	111.19	13.1	98%	246.79	62.43
16023	118.74	16.82	97%	262.5	67.56
20986	100.65	16.03	98%	269.03	97.64
23033	164.75	20.5	97%	269.22	53.32
24810	78	27.42	97%	273.76	89.28

TABLE 3G: Late Acetaminophen

Document Number 1650775

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
8592	97.92	12.74	99%	275.69	78.69
12156	66.84	25.24	99%	279.94	158.15
20555	74.21	32.18	97%	280.75	96.14
18837	70.96	24.35	98%	281.18	112.85
17758	47.9	17.49	98%	283.74	151.83
11152	89.81	23.98	98%	284.55	88.62
22582	97.84	15.79	98%	290.41	88.62
6155	86.76	17.03	100%	302.82	149.97
10093	894.21	296.81	97%	307.41	125.35
23854	518.98	43.24	97%	317.71	83.8
4314	161.66	22.27	99%	325.66	70.88
20864	896.29	162.64	98%	340.85	169.02
9072	134.11	29.83	97%	372.6	132.4
15462	187.89	20.53	99%	377.51	69.64
3023	74.88	27.06	99%	377.75	123.14
1529	196.76	20.46	97%	378.11	72.49
24670	211.91	19.4	98%	380.22	75.72
25480	139.68	36.79	97%	384.92	88.4
4224	217.33	27.1	98%	385.39	68.02
1653	161.77	30.91	99%	413.84	133.06
9905	215.17	33.74	97%	417.78	81.53
11153	184.99	26.78	98%	424.64	112.76
21977	167.03	43.78	97%	425.7	100.74
21950	225.05	28.55	97%	431.25	83.14
2505	181.37	17.8	99%	437.97	99.3
794	185.22	23.41	98%	452.2	109.84
5920	1687.13	555.96	99%	456.93	241.47
2667	266.65	38.11	98%	472.54	95.54
24722	177.21	38.39	99%	491.55	112.03
23390	1178.14	133.27	98%	504.75	225.74
1562	261.12	32.84	98%	506.49	108.81
15113	155.11	52.14	98%	515.14	163.96
4199	289.55	26.97	98%	519.47	108.02
8872	1732.12	253.22	99%	539.58	281.13
24771	204.77	35.86	99%	548.56	123.7
13088	127.47	50.84	97%	595.53	180.73
17541	1185.11	145.34	98%	686.63	152.47
24811	244.05	55.21	98%	713.37	236.19
24321	133.15	53.97	98%	767.37	279.51
7552	180.78	39.85	98%	820.01	310.92
19732	145.53	28.91	98%	918.79	410.43
11205	330.78	77.32	97%	976.22	280.85
15673	1721.01	183.17	98%	1022.66	229.71
14512	230.44	36.6	99%	1088.1	390.72

TABLE 3G: Late Acetaminophen

Document Number 1650775

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
11850	2429.93	244.48	98%	1189.68	370.45
633	647.11	128.95	97%	1346.47	304.28
14960	3443.82	469.79	99%	1352.48	446.55
22554	383.07	75.73	98%	1365.63	511.2
24049	4317.73	1756.71	97%	1441.54	440.22
2587	661.56	121.75	98%	1598.85	493.87
12314	743.43	156.24	98%	2014.22	647.46
15315	4723.83	784.41	97%	2482.27	635.01
17730	6017.72	1076.55	98%	2933.25	821.08
6189	422.42	136.09	97%	2994.06	1657.8
20873	5487.66	1292.77	97%	3014.46	6409.47

TABLE 3H: Early Acetaminophen

Document Number 1650775

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21175	8.2	4.71	94%	28.82	12.57
7528	8.32	4.93	95%	34.66	16.43
20282	-15.7	9.27	92%	36.02	33.93
5966	-2.42	11.53	95%	36.31	21.84
22695	10.13	6.89	92%	38.79	17.51
15634	1.39	5.65	94%	39.68	19.47
1520	15.99	5.3	94%	47.93	19.37
16524	20.02	6.63	94%	48.44	13.24
18482	16.24	5.44	95%	48.47	17.05
2280	19.83	5.96	93%	49.02	23.16
19787	15.18	6.28	94%	50.55	15.04
18584	6.53	10.13	95%	51.53	23.14
13926	21.46	6.96	92%	52.65	14.76
11423	15.02	8.15	94%	56.28	19.95
11940	21.79	9.2	93%	57.53	15.9
23000	22.53	12.08	93%	57.77	15.01
3080	-6.92	14.95	93%	58.31	48.7
23710	158.41	53.72	92%	58.38	71.02
23047	15.29	11.17	95%	58.49	16.56
16566	17.77	6.03	98%	58.51	15.69
19650	-70.3	47.02	93%	61.72	44.09
15467	11.36	7.01	95%	62.46	46.17
16728	14.72	12.75	92%	64.03	32.75
13568	28.12	10.02	94%	67.08	17.03
13932	-112.44	63.3	94%	67.38	48.47
15139	21.25	9.99	96%	68.11	25.84
24079	25.3	8.6	95%	69.08	26.17
22487	6.73	8.7	98%	70.08	41.42
14139	19.82	7.55	95%	71.65	22.54
15181	26.59	10.69	94%	79.78	30.61
23077	38.94	17.17	92%	81.22	21.14
17158	17.52	10.77	94%	83.01	45.36
20971	43.32	10.04	92%	83.29	21.37
1169	27.52	12.64	92%	83.96	30.23
16871	19.55	12.49	93%	85.46	26.85
9164	27.2	10.23	95%	85.81	27.4
15980	26.43	18.24	93%	86.7	23.87
16361	43.56	12.22	92%	91.15	25.64
21321	27.09	14.56	93%	105.32	56.02
3486	34.72	10.49	97%	107.9	41.25
2727	45.87	10.75	92%	110.53	48.76
8597	69.34	16.36	93%	116.43	40.21
574	65.57	6.51	93%	117.45	179.89
8730	45.4	17.81	92%	119.22	42.05

TABLE 3H: Early Acetaminophen			Document Number 1650775		
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
13351	36.93	12.29	95%	122.54	50.81
6330	28.64	17.18	98%	123.06	58.01
18829	33.89	17.14	94%	128.07	58.85
16134	18.36	24.36	94%	128.31	40.65
20975	70.64	13.75	93%	135.77	31.44
64	64.42	13.23	93%	141.31	35.51
11426	36.73	16.99	94%	143.85	61.64
4127	42.82	25.2	92%	147.26	55.78
2043	94.32	14.17	93%	149.89	35.38
25814	49.58	15.47	93%	150.18	60.26
23044	256.5	54.33	94%	154.34	33.61
23491	80.29	14.78	92%	156.45	57.06
21909	77.01	15.95	92%	157.72	48.89
16364	54.12	18.74	92%	161.04	68.62
6861	53.34	24.76	95%	173.75	47.49
23709	365.56	102.97	92%	174.65	139.26
18981	80.53	12.18	98%	180	124.54
18136	92.28	22.73	96%	180.63	44.47
15170	63.67	31	93%	182.69	57.04
15491	50.3	18.75	94%	184.71	62.38
13640	81.51	25.5	94%	194.43	69.6
1542	110.94	15.7	93%	202.72	68.33
23711	965.1	437.75	93%	203.15	366.12
3549	100.08	20.01	93%	203.26	64.36
5749	105.17	17.76	96%	203.46	50.97
1921	469.15	75.54	94%	203.88	88.71
5953	1395.67	589.94	92%	204.16	203.2
11179	51.98	16.53	97%	213.56	68.01
17571	121.22	22.36	91%	215.28	47.28
1919	540.5	142.58	94%	224.99	91
16449	-17.52	49.15	92%	225.71	118.83
7927	58.81	47.71	94%	235.03	77.05
8735	104.51	40.55	92%	260.2	118.96
15070	64.72	20.64	92%	276.22	127.77
23606	645.68	142.54	92%	308.45	97.73
4291	55.74	33.3	95%	309.48	143.72
6366	132.6	38.47	93%	309.95	143.06
22862	102.99	68.89	92%	331.29	84.1
1920	699.35	125.66	94%	334.22	116.2
23230	101.11	53.57	94%	347.39	161.95
1802	68.01	68.24	93%	348.21	129.62
1501	135.65	55.72	93%	359.59	120.35
3143	180.22	37.55	93%	360.43	101.81
20799	195.78	28.73	95%	368.39	68.29

TABLE 3H: Early Acetaminophen

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21980	205.1	26.69	96%	380.01	105.72
4234	728.11	88.4	91%	441.47	146.01
16215	277.82	31.3	92%	468.47	103.74
25705	303.85	36.79	95%	471.16	88.31
164	290.9	32.23	97%	476.12	84.6
21097	844.93	124.78	93%	521.05	142.52
23139	297.32	105.82	94%	614.3	226.46
8549	197.64	79.57	92%	674.01	251.68
9190	372.68	47.07	94%	1016.16	415.34
6291	552.9	84.63	97%	1091	307.85

TABLE 3: Late Carbon Tetrachloride					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
17064	50.24	16.97	96%	-4.18	20
1625	114.41	34.24	99%	0.07	12.89
5885	38.36	18.29	97%	1.99	9.82
18046	46.73	12.92	99%	2.71	14.04
16649	220.02	92.9	99%	3.43	37.53
1554	47.01	20.46	98%	4.33	6.64
20950	54.4	13.02	98%	6.19	12
13458	58.51	18.25	97%	6.84	20.17
6879	53.86	20.46	98%	10.45	8.61
2065	77.67	43.56	98%	14.07	10.39
16654	153.26	64.25	99%	14.11	9.91
23651	330.28	228.17	97%	21.42	37.58
15312	116.71	36.41	96%	25.99	29.2
21818	119.6	30.36	97%	26.66	21.99
4048	1573.97	2042.27	100%	28.72	92.76
21695	174.77	50.28	99%	30.87	22.35
1126	93.96	18.28	98%	31.78	16.86
17157	116.08	34.36	98%	33.37	18.38
21586	155.13	41.01	98%	35.85	31.46
4097	202.62	143.18	96%	36.77	20.82
20589	204.58	80.85	99%	39.66	14.51
4856	195.72	58.45	98%	44.87	22.87
17500	1.65	7.49	96%	45.77	44.45
16730	154.98	38.01	97%	46.39	26.25
20449	440.43	164.04	98%	47.45	46.4
15655	237.45	149.71	98%	48.19	26.25
19040	396.02	114.12	99%	54.95	29.77
1037	191.13	61.49	99%	55.16	22.83
4178	263.2	73.51	99%	58.46	46.4
23302	134	32.72	97%	60.71	24.04
21060	195.49	44.63	99%	66.73	22.3
2781	300.75	90.51	100%	67.08	21.7
1571	306.34	84.06	98%	69.24	44.27
1258	201.18	53.89	99%	69.76	26.45
20755	315.54	99.4	98%	70.92	37.08
21416	180.67	33.54	98%	71.26	32.81
4327	209.63	44.69	97%	73.46	30.98
2853	243.76	74.49	99%	79.5	27.62
14458	462.45	169.29	97%	79.77	81.9
17956	135.44	24.53	96%	80.41	19.61
16650	335.98	95.22	99%	82.71	42.71
8152	184.75	44.1	98%	84.34	21.12
22321	565.88	166.7	98%	90.43	44.8
20801	244.26	53.66	97%	93.54	45.27

TABLE 3: Late Carbon Tetrachloride			Document Number 1650775		
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
15203	217.53	41.56	99%	94.08	22.2
16683	214.61	51.64	98%	96.97	26.38
7690	485.59	136.48	97%	98.07	100.2
18705	230.49	55.83	99%	103.84	19.16
574	566.67	151.26	99%	104.84	163.13
20644	284.09	69.38	96%	104.86	53.3
12613	385.02	81.17	98%	105.74	49.08
23173	527.13	156.81	99%	112.95	62.38
10016	305.83	117.64	98%	113.41	37.12
25257	401.37	69.21	98%	123.93	52.05
19377	245.39	39.45	98%	124.66	31.89
25313	368.62	55.36	99%	125.11	47.2
23888	323.47	71.72	99%	127.05	34.78
17754	280.21	65.27	98%	127.56	39.49
20891	284.25	57.73	96%	128.54	57.37
19241	305.11	61.55	99%	128.91	25.25
17369	251.93	28.1	96%	130.99	61.88
4049	1800.21	615.67	99%	131.28	173.33
4426	226.63	33.81	98%	134.21	26.79
15282	495.77	127.65	97%	140.76	88.42
20849	288.07	45.99	98%	148.97	33.86
17225	314.55	56.91	96%	156.73	51.3
24388	756.8	218.92	98%	158.69	122.1
16854	274.55	32.55	98%	161.83	29.13
16610	376.93	79.48	97%	165.18	49.27
6193	447.67	59.78	99%	194.57	54.15
3549	368.01	54.43	97%	196.19	60.45
2744	487.89	65.94	98%	202.98	55.42
15281	509.13	65.19	98%	207.9	69.15
17571	337.5	57.58	97%	209.52	44.91
8928	323.46	31.08	98%	210.05	36.77
25802	411.96	57.18	98%	210.79	57.41
12551	48.43	13.62	98%	212.69	71.68
7602	453.04	80.74	97%	213.06	62.29
15543	555.28	110.77	97%	219.06	83.33
958	492.73	90.77	98%	234.42	59.68
2854	520.08	129.87	99%	239.21	54.99
5331	517.46	66.57	99%	253.08	62.49
23013	631.62	255.14	98%	253.69	77.98
19768	497.6	88.61	97%	258.31	86.39
18107	475.79	86.06	98%	270.37	50.73
10306	537.72	79	97%	270.7	72.51
3138	773.53	129.57	99%	280.59	128.8
16684	591.01	105.06	98%	303.32	77.67

TABLE 3I: Late Carbon Tetrachloride					Document Number 1650775
GLGC ID	Group Mean	Group StdDev	LDA Score	Non Group Mean	Non Group StdDev
23854	563.93	104.51	97%	314.55	77.09
20897	602.65	120.81	96%	315.7	85.83
19298	835.39	188.74	97%	328.8	152.97
25718	579.2	77.87	98%	328.95	68.42
14959	676.74	116.99	97%	377.46	94.35
20879	73.93	55.35	98%	390.34	126.05
6824	1794.5	585.37	97%	479.02	298.25
13684	1052.78	207.71	96%	578.09	181.33
16438	1299.24	155.02	99%	582.93	144.92
4193	332.28	95.67	96%	726.26	144.3
7552	163.75	89.31	97%	826.93	304.52
16883	681.46	275.09	96%	1856.78	528.87

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TABLE 3.J: Early Carbon Tetrachloride					Document Number 1650775
GLGC ID	Group Mean	Group StdDev	LDA Score	Non Group Mean	Non Group StdDev
8663	721.93	225.97	97%	-87.65	146.96
8662	653.64	143.71	99%	-66.58	95.42
1727	348.89	185.42	95%	-57.26	75.16
11493	129.55	67.26	96%	-32.97	39.87
2628	251.75	147.92	96%	8.65	34
15647	109.5	26.81	94%	11.25	155.64
13265	78.29	37.64	97%	12.05	9.28
923	199.22	94.23	95%	15.81	23.49
8661	614.42	215.98	99%	16.84	60.47
7301	187.05	149.7	95%	19.02	15.94
15312	129.52	34.52	94%	23.98	24.69
1305	159.8	80	94%	27.12	24.91
1598	232.56	58.02	96%	28.01	58.64
23567	918.41	595.26	94%	30.79	97.73
25198	145.62	46.46	97%	31.18	21.37
22443	413.57	187.24	96%	32.31	38.97
809	170.72	83.79	94%	33	26.32
18043	157.01	66.2	95%	35.05	27.16
16825	86.21	14.87	95%	36.95	15.49
11494	365.78	87.61	98%	39.57	52.58
12969	315.69	145.09	97%	39.62	30.17
347	94.32	20.45	94%	44.31	19.5
15313	188.23	47.79	95%	44.81	34.49
25907	196.63	51.46	96%	45.95	29.69
2629	258.22	130.51	94%	47.27	31.18
4119	172.99	53.46	96%	49.1	27.57
15617	131.28	26.96	94%	49.13	28.01
11483	356.15	129.53	95%	49.85	57.22
25098	263.21	101.83	95%	51.71	35.09
8664	685.72	187.22	98%	51.77	117.57
7806	173.92	56.36	95%	51.78	24.26
5932	142.26	26.26	94%	51.91	24.37
18501	128.83	31.95	94%	53.7	17.47
352	306.66	117.09	94%	53.93	48.46
3831	120.45	24.02	95%	55.42	25.76
651	234.03	95.8	96%	55.88	31.26
650	252.68	84.65	96%	57.08	37.09
17337	140.87	38.01	95%	60.97	56.3
7036	176.78	42.65	98%	62.22	22.87
22124	125.04	23.89	94%	64.53	17.38
23587	208.43	60.7	94%	66.37	32.19
21130	369.23	131.33	98%	72.63	40.41
353	475.4	152.81	94%	76.96	69.6
1183	426.68	140.86	99%	78.14	33.96

TABLE 3.J: Early Carbon Tetrachloride				Document Number 1650775	
GLGC ID	Group Mean	Group StdDev	LDA Score	Non Group Mean	Non Group StdDev
16080	464.2	128.58	94%	81.55	87.93
18349	210.66	61.07	98%	82.84	26.6
19184	623.72	284.24	97%	83.93	71.71
2788	214.08	67.37	95%	87.98	29.5
15291	225.71	67.73	96%	89.73	24.64
21380	195.27	36.2	95%	90.84	24.55
17908	489.98	67.94	99%	91.5	64.42
1475	764.62	270.51	94%	95.88	162.38
354	549.22	181.76	94%	96.35	76.24
14424	1887.85	604.98	95%	104.46	294.14
23438	233.78	45.73	94%	105.37	42.63
19085	235.47	46.91	96%	105.97	34.08
16318	569.79	137.14	98%	106.93	68.65
19641	354.6	119.72	94%	111.15	52.02
2049	351.74	96.17	96%	113.35	54.16
22625	588.59	137.7	98%	119.99	73.04
15616	363.79	100.12	94%	126.33	57.91
16081	590.52	148.03	94%	131.04	114.9
1306	354.57	112.94	96%	131.39	47.78
5489	361.63	79.95	96%	135.76	55.44
19086	312.97	47.23	96%	137.05	43.97
22681	1733.5	1045.76	94%	138.8	233.99
25567	440.46	120.5	94%	146.39	68.31
5820	392.73	112.42	94%	148.03	58.75
19075	541.95	182.12	95%	149.36	55.34
8314	4119.47	2769.99	98%	151.41	501.27
24234	520.49	130.96	97%	152.5	60.67
15490	337.2	71.58	94%	153.12	62.58
18259	558.61	152.63	96%	160.23	83.57
4952	867.67	202.68	94%	163.05	167.45
20795	498.26	84.68	97%	165.95	99.22
15292	331.21	64.99	94%	168.13	43.41
17735	616.97	206.23	95%	170.62	159.27
15382	2086.55	655.12	96%	179.06	342.56
6892	472.18	95.02	96%	185.03	58.03
10019	573.47	205.58	98%	186.54	69.46
8984	284.45	40.11	94%	186.61	41.02
3587	1589.64	832.55	95%	189.25	164.29
23331	343.71	75.44	96%	197.53	41.31
17753	422.58	107.22	94%	199.72	55.6
3430	482.45	99.02	96%	205.47	61.75
5937	398.98	79.16	95%	210.95	55.18
15091	457.85	75.14	94%	214.95	79.48
2615	475.24	65.04	95%	217.68	61.55

TABLE 3J: Early Carbon Tetrachloride				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
22177	437.19	83.23	94%	220.99	76.02
15558	421.96	49.45	96%	261.21	89.18
15171	2476.94	637.89	99%	267.37	221.89
24235	651.38	135.2	94%	281.24	89.88
15172	1130.82	386.63	99%	294.17	160.06
8665	2451.27	808.98	94%	320.3	582.92
3816	941.08	189.07	97%	375.12	97.06
15051	1917.64	600.05	97%	421.84	274.9
6321	1227.19	294.21	96%	436.54	171.1
11495	1157.08	222.69	95%	479.89	170.9
19012	1131.9	195.46	95%	491.44	164.34
3139	3078.65	1586.03	96%	683.5	401.95

TABLE 3K: Late Cyproterone Acetate			Document Number 1650775		
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
25183	57.99	11.18	99%	-65.21	41.14
9969	66.32	43.47	97%	-28.99	30.94
19292	39.25	15.99	99%	-0.31	8.76
1749	36.95	4.96	97%	6.56	12.85
9697	56.57	15.67	98%	10.84	13.14
19465	72.95	28.72	97%	20.05	13.1
15441	57.11	16.22	98%	20.18	10.67
15987	363.79	45.36	100%	34.51	32.07
13580	0.18	7.99	96%	36.01	21.03
16319	89.11	16.96	97%	40.72	16.75
3510	7.29	10.94	97%	41.17	13.42
906	86.53	14.25	98%	49.56	12.1
19053	13.57	5.47	95%	50.36	50.88
5824	209.96	52.5	99%	54.58	27.78
17685	17.67	8.55	98%	59.93	29.82
4588	22.45	6.38	97%	60.62	24.09
14250	25.11	4.35	96%	61.29	33.6
17091	228.81	44.44	99%	65.14	36.75
4312	458.51	102.72	98%	74.88	65.39
6667	35.58	7.42	95%	79.42	27.4
9668	25.68	7.88	95%	82.74	43.74
17090	174.43	31.41	98%	82.84	25.5
14840	25.84	4.54	97%	84.25	56.66
18906	165.1	25.73	97%	86.57	33.68
21184	24.35	7.77	96%	88.84	44.65
11960	-21.76	29.8	98%	91.47	36.61
17092	282.98	55.61	99%	100.94	37.11
18316	41.41	4.56	96%	101.42	51.02
11724	26.29	6.1	97%	107.83	53.24
21238	29.51	14.62	96%	107.94	65.27
9015	50.88	4.22	97%	111.21	39.72
22204	31.75	11.16	96%	111.85	67.38
21228	60.32	10.12	95%	127.7	59.24
25725	303.56	97.38	99%	127.99	39.22
3381	215.51	15.65	98%	129.07	31.01
14199	49.89	11.18	96%	129.55	63.16
12158	539.59	79.37	98%	149.3	94.76
20711	15.4	13.95	97%	153.96	115.63
25055	543.96	83.34	98%	160.37	97.11
15955	401.03	64.61	97%	167.69	104.75
10002	79.22	8.3	96%	169.5	85.35
15888	103.8	7.37	96%	174.62	107.57
23709	91.99	7.53	96%	180.95	142.33
19255	96.69	11.59	96%	191.17	81.51

TABLE 3K: Late Cyproterone Acetate					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
16124	59.91	18.31	97%	198.11	129.25
8053	55.5	21.16	95%	199.73	121.49
1796	713.84	124.8	99%	202.3	82.74
6431	44.99	10.12	99%	211.22	232.8
4576	60.8	23.4	95%	213.43	78.15
22713	83.58	18.05	96%	218.87	74.81
20803	489.88	37.25	100%	230.7	84.72
8905	129.45	13.33	96%	236.42	105.34
16780	482.97	115.87	98%	240.36	60.06
1479	143.4	14.02	96%	245.89	63.54
12156	947.53	169.32	98%	270.19	144.04
24860	762.67	137.57	99%	271.87	106.81
20744	131.35	9.57	96%	277.11	153.4
12157	890.46	241.3	96%	295.84	176.52
19256	169.36	16.84	97%	300.56	93.48
12155	849.1	121.68	98%	328.83	112.43
1795	886.32	169.03	98%	332.97	138.76
20864	838.11	192.14	98%	343.82	174.37
23032	174.66	35.02	96%	348.75	98.36
18860	658.47	93.14	97%	352.87	102.72
6801	167.82	26.32	95%	361.85	140
20915	707.08	113.27	95%	376.44	136.93
20707	836.46	117.26	98%	382.05	142.91
18473	830.53	86.28	99%	405.69	223.02
16278	872.29	116.7	98%	422.72	158.18
20041	189.58	32.85	98%	435.36	136.08
25056	1055.84	195.39	98%	435.67	129.34
20714	148.21	41.46	96%	438.15	637.41
15500	239.22	24.81	97%	456.63	119.52
15755	214.37	34.27	99%	457.32	99.49
11693	37.65	37.02	96%	462.5	345.74
15127	911.94	86.23	98%	466.74	134.84
21078	321.33	18.18	96%	470.87	98.57
19012	218.63	26.43	98%	519.87	206.37
20713	192.33	64.34	97%	523.9	200.74
8872	2206.69	222.08	99%	539.95	267.56
1551	300.22	24.52	98%	540.56	133.08
15391	748.88	48.29	98%	555.42	79.76
17541	1121.82	231.52	96%	689.41	156.88
2569	1283.55	169.03	96%	712.78	286.97
20804	2441.26	676.23	98%	723.52	393.32
12160	2592.66	403.1	99%	826.97	370.84
11644	421.94	97.8	96%	834	240.59
17788	2318.81	523.51	98%	909.78	263.72

TABLE 3K: Late Cyproterone Acetate					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
17117	1568.35	191.58	96%	1006.34	230.44
15645	474.3	53.72	99%	1085.08	601.13
6479	446.51	75.83	98%	1215.32	472.08
22266	2441.41	319.93	97%	1502.46	434.41
21798	2671.47	378.77	98%	1532.27	351.77
1957	451.84	140.88	95%	1533.47	786.6

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TABLE 3L Early Cyproterone Acetate

GLCC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
12375	39.55	6.91	93%	6.16	21.17
2803	101.95	30.32	98%	12.74	30.67
18685	55.02	18.44	95%	16.95	33.49
15162	38.84	5.14	93%	19.37	14.99
10200	71.52	14.25	98%	21.52	18.12
11619	40.76	5.29	93%	24.39	9.81
5018	43.56	9.08	93%	25.12	11.36
11125	95.81	17.05	97%	28.28	20.68
25706	108.93	17.96	98%	28.74	24.94
17506	202.1	34.4	99%	28.98	70.24
25852	57.42	8.81	96%	29.52	10.16
16783	107.34	24.04	95%	33.35	33.97
4725	93.9	10.69	96%	40.84	123.37
15097	97.88	13.08	95%	42.76	28.79
2594	115.78	19.67	97%	43.16	28.35
18484	139.66	35.48	98%	43.46	17.72
7967	80.61	8.41	93%	45.01	25.09
15251	113.13	7.4	98%	45.58	23.44
14913	104.39	13.3	94%	51.71	28.53
15655	103.19	9.18	98%	52.4	44.96
5740	98.42	10.02	93%	54.17	22.49
15433	88.27	7.53	96%	55.12	26.88
6676	81.6	7.48	94%	55.36	26.6
12203	284.85	67.35	98%	57.37	50.59
11876	164.99	37.72	97%	59.91	38.15
24051	156.13	27.52	97%	60.29	28.94
24227	159.76	22.26	98%	64.47	29.99
23160	140.18	19.33	94%	79.22	46.25
24236	118.22	13	94%	79.8	46.11
5754	354.87	77.25	99%	82.05	52.7
5046	201.39	29.93	96%	91.8	52.22
4679	155.83	15.02	94%	93.09	39.05
2372	227.9	45.92	97%	99.62	37.53
466	147.74	16.09	93%	100.97	24.77
9128	497.34	121.83	99%	101.85	43.69
16087	72.43	6.68	96%	105.7	17.95
22898	203.84	9.33	98%	107.87	73.23
22717	160.84	13.59	94%	114.08	91.92
9775	472.31	82.29	98%	118.73	84.58
19605	335.27	35.78	99%	131.91	48.58
22503	297.45	72.36	96%	134.1	70.26
1903	323.28	80.7	97%	134.88	55.57
6582	298.97	43.04	96%	137.13	83.58
15030	175.94	7.66	94%	138.35	50.24

TABLE 3L Early Cyproterone Acetate

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
18235	287.07	66.63	97%	138.94	38.25
15282	203.3	21.11	94%	148.94	105
13799	391.75	74.97	99%	152.36	52.97
17955	257.17	57.57	93%	154.46	62.37
6272	415.31	82.23	98%	157.51	61.87
3266	238.25	22.7	93%	160.5	50.15
15959	389.2	63.99	97%	164.9	67.38
1884	191.9	7.86	93%	166.42	45.16
15955	294.4	26.85	95%	169.12	106.78
9486	468.68	91.29	94%	177.99	126.67
21275	349.64	80.81	96%	178.44	97.42
16053	311.13	32.05	96%	206.21	223.6
16747	445.78	87.8	96%	210.09	78.61
20350	393.34	72.05	94%	217.18	69.07
6855	290.54	8.31	95%	227.55	64.59
2326	437.32	39.57	98%	229.27	188.62
20063	579.31	78.7	98%	232.67	92.42
11403	386.09	85.89	93%	235.8	240.72
14303	381.51	38.02	94%	240.55	89.2
5696	167.33	17.35	93%	246.96	110.75
7586	568.83	104.54	95%	247.96	137.64
6821	667.02	106.37	96%	253.55	163
12956	525.48	76.44	96%	256.59	86.57
11404	487.51	32.83	97%	257.84	173.77
4092	428.51	31.72	96%	269.02	120.09
20	182.6	13.17	93%	280.26	77.1
7003	480.07	48.06	93%	299.91	136.85
22835	515.95	104.87	95%	316.8	87.86
22235	511.17	15.69	98%	321.64	119.46
1900	909.26	49.41	99%	339.05	159.22
9674	997.96	198.11	93%	345.29	332.5
2757	553.61	62.46	93%	349.8	112.21
3233	469.14	29.71	94%	350.16	111.19
4937	644.14	96.95	97%	351.09	99.81
16688	485.77	14.98	95%	367.52	115.86
8215	528.57	63.29	95%	395.11	169.02
23515	527.7	47.35	94%	399.57	182.28
22548	1110.25	157.18	97%	429.36	198.23
25056	701.5	107.45	94%	439.98	142.37
23030	298.12	25.05	94%	443.27	320.1
1930	795.75	79.48	96%	488.29	180.53
22379	987.52	105.4	98%	497.46	281.53
18280	625.22	42.6	95%	500.51	355.18
13557	431.55	35.49	94%	598.3	181.76

TABLE 3L: Early Cyproterone Acetate

GLC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
1901	1382.54	291.7	97%	621.54	268.35
16205	433.92	33.39	96%	622.45	128.79
19069	172.52	18.28	97%	622.95	345.06
22906	1189.14	110.88	96%	633	508.28
7262	974.62	93.19	94%	656.38	287.35
2354	1225.56	104.8	96%	666.98	252.59
7362	563.59	37.8	94%	816.77	299.68
15345	1802.55	235.04	95%	907.53	318.35
3803	1252.52	61.21	95%	914.67	209.78
22929	620.51	53.83	95%	1008.19	813.54

TABLE 3M: Late Diclofenac					Document Number 1650775
GLGC ID	Group Mean	Group StdDev	LDA Score	Non Group Mean	Non Group StdDev
22513	2558.9	1121.55	99%	-137.91	262.53
19512	46.17	16.3	99%	-20.41	27.06
8700	150.91	57.74	98%	-11.7	37.23
19715	70.75	11.06	98%	-11.14	18.14
11645	79.3	16.37	99%	-10.24	29
20200	64.31	15.52	98%	-7.94	37.09
7858	64.65	32.07	99%	-1.01	21.41
22516	230.66	81.61	99%	0.06	50.52
18974	52.85	14.89	98%	1.86	14
5291	56.16	15.92	98%	7.46	12.49
9977	33.87	1.2	99%	9.6	16.15
372	53.19	3.15	99%	10.58	12.35
14400	168.71	36.04	98%	12.55	47.33
955	44.09	5.41	98%	13.21	12.09
26320	148.57	67.07	98%	20.83	30.04
23555	177.11	52.37	99%	22.61	21.13
10790	-147.58	11.69	99%	23.65	51
21445	152.54	38.45	99%	24.94	41.96
16173	102.32	21.29	99%	25.18	32.39
25052	653.33	363.97	98%	29.48	65.56
3452	158.59	24.76	99%	29.79	27.82
12277	126.55	32.95	98%	30.14	31.31
16240	-1.46	1.38	98%	31.65	28.31
22512	280.38	149.23	99%	44.34	59.45
7056	-11.07	4.54	99%	47.11	28.14
19411	117.91	13.87	98%	47.27	27.38
6198	184.84	21.67	99%	47.55	71.13
25246	17.4	2.21	98%	50.19	18.57
15504	223.77	86.68	98%	54.96	108.78
22514	404.55	221.07	99%	61.23	63.25
13045	-1.13	17.95	98%	64.8	29.82
9826	-2.67	5.61	99%	66.89	26.12
8079	-12.12	4.26	99%	70.37	43.83
2310	520.93	356.23	98%	71.67	85.7
25290	159.42	12.09	98%	74.09	78.6
1430	-67.02	9.22	98%	76.13	70.5
13895	199.32	16.84	98%	81.85	53.19
11904	162.22	8.31	98%	82.4	38.06
11596	208.15	21.91	98%	92.32	36.27
22515	1549.73	711.86	98%	100.85	133.92
22321	175.23	33.28	98%	101.48	89.03
8522	399.56	124.51	99%	108.85	69.48
14491	261.16	27.37	98%	115.78	52.28
21228	330.87	20.94	99%	125.87	57.45

TABLE 3M: Late Diclofenac

GLGC ID	Group Mean	Group StdDev	LDA Score	Non Group Mean	Non Group StdDev
20529	887	406.86	98%	137.26	107.43
3250	366.5	30.94	99%	144.45	58.3
14504	691.37	422.61	99%	151.43	95.9
26133	549.15	106.67	98%	153.02	280.02
21978	81	5.94	98%	160.08	42.54
3708	397.54	42.39	98%	161.72	77.01
396	355.91	58.85	98%	172.48	57.78
23889	72.55	12	99%	175.14	49.66
12577	1097.35	411.24	98%	176.09	109.22
18580	822.77	189.24	98%	201.23	172.81
24237	928.14	321.39	98%	219.99	132.72
25618	180.02	2.6	98%	245.62	81.24
4969	1833.13	949.96	98%	265.19	240.61
5110	738.94	147.68	98%	271.77	107.36
25619	193.88	2.98	98%	274.38	108.29
13353	101.42	6.77	99%	275.78	68.9
7225	610.95	103.39	98%	276.52	112.14
1175	89.72	12.52	98%	319.98	143.49
4314	199.22	16.19	98%	324.04	72.64
21281	119	14.89	99%	329.77	91.62
699	744.08	166.35	98%	385.87	84.98
17281	191.29	11.48	99%	407.86	108.78
7697	126.05	9.16	99%	418.46	147.54
24012	650.52	28.61	99%	423.59	476.52
5339	1561.45	746.53	98%	471.48	259.27
1561	1103.42	310.4	98%	483.63	109.78
24228	1037.63	336.37	98%	510.12	105.18
5616	1252.37	399.53	98%	617.19	131.84
15189	2393.48	562.64	98%	642.89	398.85
563	1286.12	293.65	98%	647.49	154.22
19392	1380.71	448.01	98%	669.42	123.39
21740	2258.4	588.09	98%	701.14	280.06
1854	2250.76	618.07	99%	730.54	265.59
3292	2871.21	931.15	99%	892.15	311.65
22598	2831.24	966.7	98%	1051.05	357.55
21661	2797.22	982.49	98%	1087.36	376.19
21660	4837.56	1684.22	98%	1692.71	582.02
17167	4555.27	1157.69	98%	2481.92	715.65

TABLE 3N: Early Diclofenac

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GLGC ID	Group Mean	Group StdDev	LDA Score	Non Group Mean	Non Group StdDev
10667	411.83	248.79	97%	13.74	165.12
17695	47.26	305.83	96%	15.36	60.09
3452	91.31	23.32	97%	29.73	28.67
21421	5.58	8.51	95%	31.49	16.56
6222	-12.72	9.64	95%	32.02	30.46
14996	180.85	117.09	98%	32.69	45.29
12844	-11.84	8.74	96%	39.54	27.67
1843	88.96	20.57	96%	48.67	17.77
9635	-9.83	19.06	95%	48.68	40.62
21707	169.82	64.58	95%	59.13	53.37
23302	37.52	28.79	96%	62.8	26.58
13932	-63.25	79.49	95%	63.9	55.2
18604	24.17	7.4	97%	65.08	25.49
20354	220.66	86.86	98%	66.15	50.9
1841	188.63	53.81	95%	69.83	46.13
355	149.37	52.24	97%	71.24	34.86
17683	40.01	12.49	96%	77.75	25.92
2359	17.87	8.17	98%	86.55	44.73
3713	168.44	419.14	97%	89.98	96.34
11840	51.82	10.03	96%	100.7	37.97
19211	88.71	85.04	96%	108.71	56.23
17800	70.19	39.86	98%	118.7	28.58
1844	277.5	69.37	96%	129.25	44.39
356	249.59	82.38	98%	129.82	46.84
23494	49.03	10.06	96%	131.42	50.45
14776	49.01	22.62	97%	134.61	47.31
23626	251.41	69.01	97%	141.32	90.59
23491	85.95	100.32	96%	155.17	56.53
21382	60.1	10.48	95%	162.86	70.74
6213	75.91	24.03	97%	177.43	53.8
15170	66.01	17.61	95%	180.78	58.76
23182	47.61	14.34	95%	182.97	82.24
14958	77.51	24.88	99%	192.52	57.74
16562	315.91	84.36	96%	194	49.14
23043	116.23	50.3	97%	200.45	58.35
18996	115.11	26.79	96%	211.48	69.45
14997	807.1	529.54	98%	231.67	129.71
10879	84.17	41	95%	235.09	83.29
11021	90.03	69.2	95%	247.67	106.37
2655	43.2	16.5	97%	258.1	178.54
16859	704.09	252.4	97%	258.84	124.37
17794	130.88	63.44	97%	261.13	86.21
6919	1235.49	468.87	99%	269.17	229.63
13353	151.45	114.9	97%	276.39	67.85

TABLE 3N: Early Diclofenac

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
20	432.75	81.44	97%	277.59	75.26
12964	106.32	33.26	95%	288.44	95.46
3722	585.01	101.14	97%	295.66	101.48
20715	308.31	50.21	96%	313.11	180.79
23606	668.08	172.75	97%	313.49	105.76
23230	176.98	99.78	98%	342.52	164.69
12946	142.18	31.13	97%	349.51	100.28
24200	1265.26	395.08	97%	369.8	208.75
16768	264.62	55.65	95%	376.13	78.38
12857	231.61	293.1	96%	392.81	143.31
18795	726.51	149.33	97%	395.27	107.88
19	654.92	135.45	97%	397.11	105.29
18783	716.54	157.61	95%	402.03	119.63
19252	288.39	79.84	95%	410.59	104.1
1114	645.09	101.99	96%	427.86	137.39
20698	914.65	381.61	97%	479.92	178.44
21098	1119.71	394.89	99%	521.35	157.69
21097	883.9	345.03	98%	525.66	142.61
15191	1868.16	232.88	99%	528.3	355.46
19373	957.63	171.61	96%	529.59	254.13
9424	1020	141.63	96%	537.58	150.22
15606	331.04	100.93	95%	555.14	142.5
4670	2609.57	936.24	97%	576.03	466.99
402	1115.89	448.86	99%	596.85	131.13
13557	267.85	27.9	96%	601.37	178.89
2368	429.73	38.72	96%	606.25	88.63
22906	2134.54	974.52	97%	617.58	470.92
15189	1986.69	445.74	98%	635.58	391.8
15190	2159.12	392.22	99%	661.42	378.72
1995	1259.5	439.49	98%	684.23	244.32
11830	1983.61	566.45	98%	692.89	304.27
1805	1229.6	164.21	97%	703.35	218.45
1174	1340.59	440.4	96%	726.33	411.01
6013	1139.77	436.67	96%	749.39	184.56
17785	1846.83	672.05	97%	752.99	445.33
22840	1352.3	529.97	95%	755.78	273.45
8515	346.51	83	96%	785.99	292.49
21574	391.95	100	97%	817.75	226.02
6477	1367.6	542.86	97%	857.33	304.69
3292	1879.44	784.97	98%	890.76	323.1
12306	3293.83	1170.7	99%	1005.26	433.69
7451	1583.77	483.79	96%	1014.48	337.6
6295	2775.87	1040.34	99%	1068.45	493.12
21467	2391.61	1040.88	96%	1118.01	516.67

TABLE 3N: Early Diclofenac

Document Number 1650775

GLGC ID	Group Mean	Group StdDev	LDA Score	Non Group Mean	Non Group StdDev
6633	2355.01	832.32	99%	1206.88	312.71
14738	2426.79	883.37	99%	1231.22	312.92
3730	2978.69	1180.6	98%	1232.87	586.1
3617	2869.63	1011.46	98%	1268.73	398.2
8715	3069.61	1101.03	99%	1353.63	759.44
17672	2889.9	351.84	96%	1930.21	397.38
26152	5392.56	2027.73	98%	1991.62	852.89
20846	4030.03	570.84	96%	2449.47	889.44
6018	11859.37	4320.03	98%	3477.55	3126.6

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TABLE 3O: Estradiol

Document Number 1650775

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
19476	221.25	108.8	94%	-58.59	73.88
20579	65.59	26.23	87%	-13.8	30.61
4520	74.3	35.09	90%	-1.56	34.15
55	34.69	14.89	86%	4.7	13.41
384	44.98	13.2	86%	5.76	28.49
22722	566.51	262.91	96%	19.66	47.88
12120	291.19	164.4	93%	20.32	48.27
16283	59.56	11.97	91%	25.04	15.43
10611	78.35	19.48	91%	26.01	28.58
3570	1203.99	486.89	96%	27.26	139.67
3929	66.1	15.81	88%	32.04	17.87
16783	94.16	35.66	86%	32.29	33.01
6604	9.87	7.84	88%	36.24	17.57
10540	70.62	15.26	85%	39.69	19.11
3846	63.36	11.22	85%	40.64	15.95
14266	463.56	161.4	95%	42	79.9
15097	-4.06	20.79	88%	44.39	28.23
16809	77.26	7.57	89%	53.84	28.46
672	185.2	45.2	92%	57.01	48.59
25290	322.26	83.7	94%	68.08	67.25
5493	104.13	22.09	86%	69.51	45.42
17699	379.25	121.82	95%	77.01	64.08
15057	178.76	62.35	89%	80.64	61.88
4082	137.71	29.22	87%	81.24	39.54
3074	305.3	91.43	94%	82.44	74.5
12655	222.74	65.14	88%	90.1	61.41
3073	404.03	113.1	94%	97.56	106.47
23220	158.44	34.05	86%	104.71	23.6
18612	214.55	48.01	88%	114.72	54.02
24442	253.1	51.52	95%	119.28	39.27
19258	345.84	102.07	91%	119.63	94.13
6789	266.72	63.61	88%	130.61	57.1
11465	687.63	230.97	94%	136.61	114.55
23491	259.04	44.02	89%	151.54	55.44
3075	515.63	145.3	94%	159.61	267.05
19261	291.37	82.45	86%	163.74	57.85
17393	223.13	34.27	86%	164.98	67.02
23987	254.16	41.43	86%	168.68	53.84
13229	314.84	68.95	90%	184.84	61.96
15295	252.4	28.26	85%	191.1	52.8
23183	91.05	26.84	85%	192.16	88.8
6549	522.38	151.13	89%	204.39	114.46
13092	440.75	124.27	92%	206.68	86.61
9402	278.52	27.55	85%	207.63	69.5

TABLE 3O: Estradiol						Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev	
23362	362.98	58.85	92%	209.03	55.26	
729	141.14	32.05	85%	209.19	55.66	
13963	572.36	193.21	91%	220.12	112.51	
17516	287.34	30.47	85%	223.48	56.14	
7927	368.05	56.64	86%	226.41	79.19	
14989	306.39	34.48	90%	229.8	59.41	
5464	608.63	139.88	93%	235.86	136.35	
14997	313.77	45.38	92%	237.05	156.21	
23337	388.86	61.57	87%	239.19	87.95	
6541	835.22	410.07	90%	240.86	107.93	
9621	349.89	41.41	91%	242.89	62.26	
18877	1770.96	536.63	95%	251.02	323.54	
19825	76.2	82.83	85%	256.34	107.9	
291	413.96	84.34	85%	256.37	66.6	
17613	349.67	47.08	86%	259.18	106.99	
19824	83.21	81.92	87%	260.01	99.57	
7684	577.91	188.77	85%	279.08	126.11	
2373	634.92	150.17	92%	285.8	133.51	
2484	57.67	44.88	86%	289.53	213.13	
16684	447.2	65.17	88%	306.67	87.7	
6975	700.83	228.78	86%	312.49	161.5	
18141	1086.32	372.55	88%	330.82	216.89	
25718	464.33	56.04	91%	331.59	76.26	
18742	172.88	37.74	87%	352.25	190.08	
12361	1014.46	256.68	94%	354.09	232.49	
16327	558.02	61.36	88%	369.06	94.06	
21164	169.42	47.37	88%	370.17	185.53	
24012	2053.62	525.68	94%	382.21	392.09	
4674	167.98	66.36	88%	452.2	224.88	
6060	310.86	53.86	88%	477.05	121.08	
1561	310.14	86.6	90%	491.78	117.97	
11227	841.6	140.02	86%	496.07	212.99	
19728	229.27	93.53	88%	501.97	174.65	
12746	759.81	83.64	93%	520.3	104.48	
12585	909.57	150.85	86%	542.79	178.84	
23437	271.75	62.16	86%	558.17	246.21	
11821	1051.26	228.29	86%	574.09	309.97	
24707	407.68	85.92	85%	598.16	183.22	
16894	1105.64	177.51	91%	731.2	332.55	
11720	397.65	148.44	88%	748.93	265	
4440	398.17	156.94	89%	804.73	210.24	
7584	2336.91	636.07	91%	819.41	712.46	
13093	2287.36	766.73	90%	825.52	505.38	
11644	485.11	142.46	86%	838.95	238.55	

TABLE 3O: Estradiol

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
9475	422.84	219.9	86%	958.81	372.8
24112	1879.78	259.59	90%	1026.22	630.45
16703	714.02	96.32	86%	1057.6	331.01
15534	1418.23	154.26	88%	1104.88	261.78
14738	862.34	156.54	85%	1256.55	349.62
14960	1831.5	294.22	85%	1370.37	509.8
22554	609.46	270.71	86%	1371.14	511.54
6015	707.01	273.93	89%	1539.98	455.17
7497	1136.4	136.44	87%	1691.66	329.88

TABLE 3P: Late Indomethacin			Document Number 1650775		
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21075	56.56	18.08	99%	-101.64	72.06
3626	270.02	126.67	99%	-91.68	41.85
20522	88.79	62.74	99%	-86.26	44.12
18203	28.03	7.89	100%	-59.65	26.67
21682	139.83	65.11	99%	-56.8	31.49
20119	75.13	51.9	99%	-51.89	22.95
945	164.01	44.63	98%	-32.43	36.01
8017	40.5	7.12	99%	-4.91	18.36
22516	427.71	48.74	100%	-3.53	27.61
7858	133.46	131.64	99%	-2.18	10.32
11731	57.13	15.61	99%	-1.13	13.51
20111	88.53	22.86	99%	5.7	10.46
19121	104.23	50.09	99%	16.77	12.76
24826	218.27	46.71	99%	17.2	179.73
23555	133.19	49.37	99%	22.23	20.8
21445	313.48	71.78	99%	22.36	29.24
1777	117.77	21.2	99%	22.67	16.4
16173	249.12	60.67	99%	23.05	21.76
21683	179.43	48.48	99%	24.37	26.58
19503	106.66	42.52	99%	24.54	12.74
19444	479	225.49	99%	26.17	29.3
20651	252.93	78.27	99%	26.84	24.52
11172	108.09	14.64	99%	27.38	25.08
7196	70.2	6.99	99%	27.5	18.37
8864	168.51	38.98	98%	28.16	40.98
25052	413.35	149.76	98%	28.65	72.19
12277	188.8	30.97	99%	28.87	27.27
20134	115.79	25.97	99%	31.07	21.72
15961	155.48	44.33	99%	31.59	27.65
22897	135.13	41.74	99%	33.43	19.08
1893	250.46	53.73	99%	40.37	21.42
22512	493.75	186.61	99%	40.54	35.84
14081	1307.16	578.37	99%	40.73	109.27
25083	96.77	17.16	99%	41.1	19.54
17500	182.9	29.18	100%	43.12	42.04
2013	191.84	31.9	99%	44.55	23.34
8273	410.92	194.88	99%	45.89	30.96
19411	184.69	32.53	99%	46.1	23.55
15504	896.04	321.22	99%	46.28	53.42
22514	543.21	150.84	99%	57.67	44.72
155	187.91	27.8	99%	62.07	21.49
20523	337.44	89.8	98%	66.71	58.22
16961	225.29	41.42	99%	71.58	40.53
24589	412.43	149.59	98%	73.14	30.15

TABLE 3P: Late Indomethacin

Document Number 1650775

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21285	903.94	338.62	99%	73.28	108.74
15503	519.54	109.49	100%	74.61	27.28
6200	1572.18	522.18	99%	78	145.78
7743	288.96	85.4	98%	83.77	52.71
2012	357.34	70.02	99%	84.87	34.39
3749	-48.1	12.54	99%	87.36	48.17
4892	2121.77	1018.81	99%	97.96	339.86
24651	168.51	30.23	98%	98.36	20.05
23005	536.62	86.56	99%	99.43	90.49
1700	273.11	39.16	99%	102.11	30.56
22898	507.42	174.82	99%	103.97	57.4
8522	552.47	146.35	99%	105.43	54.02
12714	0.7	18.22	98%	106.47	34.92
15116	243.85	52.64	98%	107.4	25.94
17277	239.1	35.46	99%	107.78	39.78
22042	21.05	10.38	98%	109.25	91.56
21414	1412.18	189.99	99%	116.04	143.33
17258	235.7	32.66	99%	120.39	25.05
682	555.72	137.48	99%	126.28	58.1
17369	441.37	64.2	99%	130.38	54.83
20529	790.13	186.87	99%	134.07	101.45
14504	773.65	116.14	99%	147.38	84.22
154	347.17	63.6	99%	154.37	37.49
12450	-60.33	24.42	99%	154.48	84.94
6431	1828.3	421.64	99%	190.99	149.33
18580	1167.73	411.76	99%	193.7	141.11
8310	107.35	13.86	99%	204.96	44.79
14330	633.28	126.05	99%	225.12	77.1
5687	48.78	22.59	99%	227.66	79.73
14185	760.34	170.85	99%	253.08	93.43
21443	569.4	110.65	99%	256.7	61.78
16519	807.19	191.58	98%	273.02	117.31
9079	820.52	184.52	98%	316.54	112.19
19469	162.04	26.75	99%	325.82	57.22
373	115.43	31.34	99%	334.03	85.91
43	156.53	22.34	99%	341.11	74.71
20864	37.65	12.15	100%	352.3	179.09
699	762.57	112.9	99%	383.6	79.72
24323	230.34	24.71	99%	398.78	95.09
17281	100.34	30.42	99%	410.15	105.21
16366	113.72	34.12	99%	439.22	103.99
21014	188.22	42.97	99%	572.37	137.02
16367	166.59	86.34	99%	612.27	144.06
25525	264.07	72.58	99%	645.12	117.62

TABLE 3P: Late Indomethacin

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
635	308.38	68.87	99%	672.17	126.74
18890	126.36	42.96	99%	679.93	361.87
634	355.69	72.95	99%	705.77	125.16
6236	227.28	73.91	98%	902.24	429.28
10984	135.85	78.66	99%	1092.48	362.92
15029	181.72	50.19	99%	1492.95	529.6
4933	357.28	114.44	99%	1702.56	598.89

099417800 = D73404

TABLE 3Q: Early Indomethacin

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21682	85.12	87.03	93%	-56.37	33.66
1510	75.53	7.54	96%	-13.1	65.66
26280	109.21	31.74	89%	-10.05	85.78
11422	60.74	22.85	91%	13.75	11.38
1507	46.96	9.51	87%	15.4	15.74
16251	34.42	5.87	90%	20.02	13.62
19671	39.81	7.46	90%	22.33	14.64
23106	48.6	11.99	93%	28.28	33.85
2736	49.82	5.14	93%	29.89	18.47
25077	111.99	30.35	88%	30.69	73.6
1221	445.47	178.19	92%	33.57	94.3
18389	94.31	16.02	94%	33.62	32.95
3972	-24.58	15.09	94%	34.18	35.89
18237	63.23	7.16	91%	36.35	20.91
22725	4.84	8.57	88%	36.54	24.3
17854	94.21	22.12	90%	48.6	21.13
25379	64.97	7.1	91%	48.71	16.47
1843	85.73	19.01	94%	48.71	17.88
4504	96.84	28.13	90%	48.77	77.49
24024	75.74	15.08	90%	50.05	33.85
16809	117.87	32.17	90%	53.62	27.39
11423	102.73	23.05	89%	54.5	20.13
2042	92.88	5.97	96%	54.98	50.98
13992	110.02	45.53	90%	55.81	24.86
22918	27.24	5.2	92%	57.51	29.32
5059	222.71	98.2	92%	61.9	61.99
20354	194.32	79.46	91%	66.49	51.97
18529	139.38	36.52	88%	68.68	53.21
8079	-1.13	28.24	91%	70.82	43.57
7176	83.8	6.04	89%	71.68	21.23
24721	116.01	17.12	91%	75.35	29.71
11904	169.62	30.75	91%	81.73	37.23
3710	-40.52	24.79	89%	84.89	112.56
1271	127.09	19.36	88%	87.87	22.54
15207	207.84	67.65	90%	88.03	53.57
21256	150.53	29.3	87%	90.66	43.12
1572	134.45	17.05	87%	92.3	26.58
19410	154.21	25.11	89%	95.44	23.68
16080	172.16	50.03	89%	95.77	117.15
17950	134.99	16.51	87%	96.23	39.64
22321	169.07	47.34	95%	101.03	89.08
9223	166.07	27.83	88%	106.75	43.32
17277	186.86	45.28	88%	108.27	41.12
16125	212.34	60.78	90%	109.55	34.54

TABLE 3Q: Early Indomethacin				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
354	156.92	39.75	88%	113.78	121.78
22151	49.94	21.66	90%	114.35	59.07
16477	205.91	47.02	87%	118.16	42.37
15884	197.78	19.66	96%	119.51	58.67
25768	189	17.68	94%	128.02	30.12
6532	275.04	58.08	92%	135.65	42.31
2555	342.38	116.88	91%	141.73	57.69
25370	95.55	12.34	87%	141.81	76.1
1426	186.05	11.71	91%	141.89	28.02
16081	293.29	79.31	90%	147.43	146.68
154	240.39	32.25	90%	155.47	42.04
1521	271.17	53.27	87%	157.16	61.75
22806	82.54	19.97	89%	169.69	77.1
1141	221.49	23.61	89%	172.77	35.13
9595	369.54	72.63	90%	176.26	67.68
21709	240.64	11.92	95%	179.9	33.86
13332	111.82	16.97	88%	187.21	61.88
21444	292.61	40.73	91%	204.56	58.9
20350	333.21	45.66	91%	216.95	69.67
3776	316.54	58.6	88%	226.04	54.29
958	283.88	16	89%	240.09	72.64
18891	63.95	40.8	91%	245.89	190.12
15786	130.41	48.25	89%	247.11	88.8
22619	509.69	128.09	87%	254.11	122.09
2655	76.89	36.89	90%	257.67	178.99
21443	408.93	75.59	90%	258.32	68.58
17664	718.76	159.35	90%	309.86	189.82
1795	179.95	54.13	87%	340.51	149.15
6825	188.01	57.66	89%	342.19	121.17
18465	583.12	68.3	93%	353.78	236.17
19412	798.48	156.59	91%	364.41	124.75
4026	854.17	324.83	92%	368.96	133.71
20915	208.25	51.68	88%	381.94	139.96
12463	631.37	114.76	89%	391.56	105.49
7122	778.65	154.65	89%	421.1	129.61
23245	695.04	100.61	88%	453.5	126.98
20701	818.5	138.91	89%	496.14	169.1
23125	203.3	56.02	88%	520.99	516.04
21740	1357.78	289.81	91%	701.6	296.47
16458	933.78	80.79	89%	722.78	196.14
11720	1393.76	333.85	92%	731.5	257.06
23449	166.05	104.49	89%	922.94	660.67
23989	1702.06	285.92	87%	1063.27	404.32
22368	637.02	202.48	88%	1081.65	343.44

TABLE 3Q: Early Indomethacin

Document Number 1650775

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
24289	672.7	120.08	88%	1097.27	342.03
16885	837.41	195.77	91%	1485.4	407.68
9267	809.11	323.93	92%	1667.39	543.29

TABLE 3R: Valproate					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
26190	239.04	44.21	99%	-115.53	71.46
2154	26.52	22.45	98%	-34	15.98
12625	129.76	35.25	98%	-7.97	79.74
4231	160.07	13.84	100%	-6.47	34.51
360	42.77	15.77	97%	-5.58	16.63
24126	127.21	24.22	97%	6.68	31.59
8993	64.31	7.77	99%	8.92	10.71
19762	168.43	71.93	99%	9.69	24.52
11336	60.09	15.29	99%	12.42	10.72
20993	73.86	17.79	98%	12.51	23.49
330	76.9	11.84	98%	13.5	26.03
12058	48.89	5.96	98%	16.85	15.53
1579	75.5	19.78	98%	16.86	13.09
5993	49.43	5.91	97%	17.56	13.02
8054	63.83	11.7	97%	17.56	15.18
23315	53.08	6.14	98%	20.16	11.05
23843	102.85	21.92	99%	21.2	18.22
11315	170.88	30.14	98%	22.9	42.27
13812	138.26	33.46	99%	26.62	22.64
23106	97.66	12.04	99%	28.05	33.33
11625	70.95	9.83	97%	28.43	16.22
9374	155.52	11.78	99%	30.44	41.52
10394	210.39	57.19	99%	35.12	29.91
6101	146.33	49.53	97%	38.17	25.87
2117	107.64	17.82	97%	43.75	19.24
12614	113.54	14.75	98%	45.51	37.01
9766	130.53	51.66	98%	47.22	33.17
2932	256.87	86.84	98%	48.26	30.66
13501	145.64	35.69	98%	48.87	22.87
14913	145.2	21.59	98%	51.42	27.75
16673	133.08	23.07	98%	53.6	21.07
2042	183.57	50.07	98%	54.55	49.7
2915	150.2	35.95	98%	55.29	23.13
19669	192.83	28.28	99%	60.25	31.79
19264	145.96	13.12	98%	62.26	25.95
17257	197.58	17.21	99%	67.22	34.6
15663	157.22	12.55	98%	67.92	42.04
11527	186.56	12.56	97%	68.89	53.83
22375	201.22	32.17	99%	75.66	28.1
5754	289.15	110.18	98%	82.52	54.48
12198	157.09	5.38	99%	83.53	37.27
18885	179.92	14.06	99%	85.54	27.13
13166	392.55	98.9	98%	89.27	56.47
13251	155.07	11.85	97%	89.73	88.96

TABLE 3R: Valproate

Document Number 1650775

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
8728	346.01	114.17	98%	90.12	40.25
2216	234.47	28.59	99%	94.87	37.16
21535	197.23	12.53	98%	96.15	38.42
21567	509.19	66.46	98%	97.9	104.57
10593	328.02	63.73	99%	101.91	43.97
17368	241.72	37.58	97%	104.44	49.02
9800	366.46	11.6	99%	105.66	68.67
17479	261.87	40.08	99%	106.14	33.44
21976	256.5	24.3	98%	106.4	45.51
14600	242.39	40.76	98%	111.36	76.44
22570	241.74	26.13	97%	111.56	44.08
23656	273.7	31.03	98%	112.56	52.23
15179	255.98	37.97	98%	112.9	41.1
16616	304.19	58.02	98%	115.37	49.86
5608	233.3	11.25	97%	122.33	53.28
20090	263.76	45.31	98%	126.59	32.66
17644	333.21	52.99	98%	128.35	68.07
15149	345.13	64.29	97%	128.59	59.92
6789	283.91	53.49	99%	133.02	59.87
6686	369.2	41.65	99%	139.06	46.36
19230	391.37	57.35	98%	149.61	84.83
13949	47.22	6.84	99%	151.24	58.29
11280	287.5	36.75	98%	159.37	38.65
19513	345.16	59.75	97%	163.49	60.93
23762	321.28	26.82	97%	164.97	66.22
13838	437.29	30.14	99%	166.7	55.87
2691	316.24	12.09	98%	168.14	70.13
9572	409.53	66.85	99%	168.33	60.29
6861	397.87	34.78	100%	168.71	47.4
22135	361.16	95.89	98%	170.63	47.21
24388	283.3	44.23	98%	172.33	155.38
18886	403.05	74.14	98%	175.49	63.14
24368	602.67	63.22	99%	183.22	79.82
5381	356.13	13.85	99%	191.57	49.01
9402	342.47	21.74	97%	208.49	68.96
17261	546.81	71.98	99%	219.95	72.35
2101	430.5	35.07	99%	224.81	67.09
24369	546.78	56.44	97%	228.98	103.39
11354	530	66.53	99%	229.49	68.24
8709	90.79	24.72	98%	233.09	61.98
24367	400.74	12.79	99%	245.59	55.58
19052	646.73	83.13	98%	254.53	92.68
22957	665.35	87.82	98%	274.44	208.86
15551	493.87	26.61	99%	304.36	63.07

TABLE 3R: Valproate

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
12317	639.88	73.89	99%	308.65	88.02
4179	845.91	78.29	98%	333.97	135.14
6440	961.78	166.32	97%	351.53	186.44
7111	553.56	43.59	98%	353.19	75.73
18285	707.67	76.76	99%	357.46	132.75
12928	791.23	86.89	98%	410.91	94.08
15051	1110.61	136.73	97%	476.75	412.42
2569	338.95	14.84	98%	721.15	290.78
3803	499.92	74.41	97%	920.04	208.7
18962	573.38	98.13	99%	1606.33	624.84
5052	906.23	65.55	99%	1930.67	442.76
22540	1108.89	178.44	97%	2311.11	657.83

TABLE 3S: WY-14643

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
3175	81.67	38.5	98%	-24.57	20
2051	31.61	16.91	98%	-19.67	25.77
23627	40.97	4.93	98%	-14.82	37.36
16409	95.86	23.34	97%	-8.25	35.38
14116	38.83	17.55	99%	-7.83	5.25
18029	208.84	94.33	98%	-7.23	21.53
6677	32.1	15.65	98%	-6.62	9.95
20856	275.88	94.5	99%	-5.26	14.41
5565	221.64	85.1	97%	17.46	47.37
12467	216.39	65.04	99%	20.32	20.78
23500	148.59	59.24	99%	22.05	17.54
1858	529	114.56	99%	23.94	68.23
8820	81.06	9.86	99%	28.61	31.53
18082	128.62	31.47	99%	29.7	16.97
4931	135.4	29.63	97%	33.8	32.95
9925	117.26	29.18	98%	42.43	17
24381	97.68	12.7	98%	43.65	17.97
6292	96.5	10.27	98%	43.76	16.97
5518	-34.55	15.68	100%	44.56	14.44
18083	370.91	74.26	98%	45.23	60.06
4272	590.58	82.76	100%	47.77	61.51
7295	114.22	11.36	98%	48.54	27.07
8315	251.82	52.39	98%	50.52	44.35
20855	205.89	56.89	100%	51.41	13.97
15018	153.93	12.99	97%	51.69	40.82
22046	173.79	36.81	97%	52.05	35.05
4438	-53.05	31.71	99%	53.83	12.81
18956	233.24	49.47	99%	57.47	28.38
3631	135.16	24.43	97%	62.18	23.06
4271	1146.85	102.6	100%	63.33	94.28
6553	215.81	43.91	97%	64.81	42.7
3558	192.81	32.74	98%	65.12	31.67
20038	306.38	66.25	98%	68.41	50.76
7517	190.58	26.66	98%	71.67	32.59
3743	185.35	31.74	99%	71.95	25.24
14507	291.71	54.52	98%	74.57	66.85
18749	288.03	90.54	98%	77.94	40.13
4290	293.68	45.21	98%	87.32	46.32
14595	321.16	55.3	98%	89.33	56.57
14264	331.35	82.51	98%	91.8	58.3
397	232.66	39.79	99%	91.99	32.22
18746	280.52	43.35	98%	93.45	48.78
3439	244.57	26.7	99%	100.37	28.67
2190	164.79	17.03	97%	100.78	189.02

TABLE 3S: WY-14643

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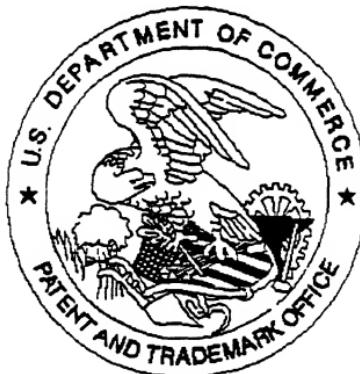
GLGC ID	Group Mean	Group StdDev	LDA Score	Non Group Mean	Non Group StdDev
18318	279.93	40.82	98%	111.57	48.48
5887	1076.32	275.73	99%	111.64	138.98
3513	212.58	33.36	98%	114.18	27.84
22416	1001.99	170.33	99%	121.52	83.97
22224	487.47	76.85	99%	124.54	72.09
12215	632.99	209.38	98%	141.79	100.45
9373	419.3	49.02	98%	144.86	76.23
15672	378.23	65.03	98%	151.17	68.05
3260	508.28	175.97	98%	153.29	72.65
16700	596.39	103.44	99%	155.05	96.4
18747	457.04	82.08	97%	155.98	76.29
26109	1286.05	121.59	99%	156.58	201.4
22737	685.5	206.71	99%	168.28	96.83
3720	315.08	30.72	98%	179.69	49.62
2113	410.43	34.36	99%	185.32	58.03
15015	374.26	31.51	99%	192.11	63.36
6439	425.56	74.96	97%	196.56	74.01
22370	945.85	62.98	100%	216.15	108.38
2457	1132.75	158.6	99%	227.31	140.2
1728	477.23	66.78	98%	227.92	60.65
18891	1245.42	225.38	99%	230.61	151.12
22620	386.56	21.42	98%	235.22	68.77
19591	567.11	40.94	99%	237.04	108.52
5602	1404.36	215.76	99%	242.82	212.8
24860	67.15	34.2	97%	279.45	115.83
22392	598.76	55.66	99%	296.04	67.51
18742	1303.27	263.5	99%	335.32	154.05
6825	626.39	47.06	98%	336.52	118
21164	991.37	155.11	99%	356.95	172.12
9372	1244.96	107.3	99%	368.29	225.64
8177	121.78	23.64	97%	389.45	423.88
17935	1404.15	220.52	97%	416.54	273.3
10533	1054.36	147.32	98%	421.36	212.4
16944	747.42	72.2	98%	422.41	133.98
21354	2186.83	317.02	98%	437.51	348.77
16323	223.57	44.79	99%	465.4	220.36
9423	273.32	30.42	98%	486.76	134.12
19044	814.58	45.86	97%	502.31	184.58
18727	206.23	25.52	99%	516.82	179.53
18125	1062.51	80.83	99%	529.14	174.32
16704	1486.63	221.63	97%	565.52	242.61
3099	922.46	83.44	97%	599.33	119.33
2813	1250.39	172.69	98%	603.02	185.25
20998	325.2	72.5	97%	606.04	134.27

TABLE 3S: WY-14643

Document Number 1650775

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21010	1699.76	218.74	98%	606.25	249.41
14882	377.63	34.39	97%	607.89	168.14
5616	386.99	47.15	97%	623.82	140.57
16945	1098.96	98.19	98%	628.67	192.67
7420	1415.94	79.85	97%	655.69	311.93
18890	1900.82	258.12	99%	657.78	337.82
3279	1571.19	374.24	98%	708.13	199.08
16190	1581.05	206.33	98%	716.2	226.42
20597	378.94	48.6	98%	742.21	189.37
21341	1797.23	203.99	98%	768.53	328.94
4940	623.22	140.4	98%	1632.44	469.8

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